

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:10:27 ; Search time 15 Seconds
(without alignments)
32.045 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_73:*
2: pir1:*
3: pir2:*
4: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	85.0	9	2 A24244	adipokinetic hormo
2	17	85.0	53	2 T00172	hypothetical prote
3	17	85.0	53	2 D89989	hypothetical prote
4	17	85.0	63	2 T29202	hypothetical prote
5	17	85.0	65	1 A32613	adipokinetic hormo
6	17	85.0	67	2 T12860	hypothetical prote
7	17	85.0	70	2 A86942	hypothetical prote
8	17	85.0	72	2 S15137	thioredoxin h2 - s
9	17	85.0	77	2 S18581	puto protein limpo
10	17	85.0	77	2 T50756	hypothetical prote
11	17	85.0	84	2 E69268	thioredoxin 2 - sl
12	17	85.0	88	2 B46264	Ig heavy chain V-I
13	17	85.0	98	2 F47624	gene E2 protein -
14	17	85.0	99	2 S37447	gene E2 protein -
15	17	85.0	99	2 S37448	gene E2 protein -
16	17	85.0	99	2 S37442	gene E2 protein -
17	17	85.0	99	2 S37444	gene E2 protein -
18	17	85.0	102	2 G71043	GTP-binding protei
19	17	85.0	102	2 B56956	thioredoxin - rabb
20	17	85.0	104	1 A28086	thioredoxin [valid
21	17	85.0	105	1 JH0568	thioredoxin - rhos
22	17	85.0	105	1 JS0667	thioredoxin - rhes
23	17	85.0	105	1 S04352	thioredoxin - rat
24	17	85.0	105	1 S04107	thioredoxin - mous
25	17	85.0	105	1 A30006	thioredoxin - chic
26	17	85.0	105	1 T33843	hypothetical prote
27	17	85.0	108	2 AH2101	thioredoxin [impor
28	17	85.0	112	2 PH0980	Ig heavy chain V r
29	17	85.0	112	2 PH0980	Ig heavy chain V r

30	17	85.0	112	2 AF2549	hypothetical prote
31	17	85.0	113	1 S57775	thioredoxin h - cyt
32	17	85.0	114	1 J02242	thioredoxin h - Ar
33	17	85.0	115	1 G3H0JN	Ig heavy chain V-I
34	17	85.0	115	2 PL0238	Ig heavy chain V r
35	17	85.0	115	2 G72642	probable surface p
36	17	85.0	116	2 T10739	thioredoxin - comm
37	17	85.0	117	2 PL0237	Ig heavy chain V r
38	17	85.0	117	2 PL0235	Ig heavy chain V r
39	17	85.0	117	2 PL0234	Ig heavy chain V r
40	17	85.0	118	1 S34812	thioredoxin h2 - c
41	17	85.0	118	2 T10170	thioredoxin - cast
42	17	85.0	118	2 S58118	thioredoxin (clone
43	17	85.0	118	2 S58120	thioredoxin (clone
44	17	85.0	118	2 PL0231	Ig heavy chain V r
45	17	85.0	118	2 F82424	Ig heavy chain V r

ALIGNMENTS

RESULT 1
A24244
adipokinetic hormone - bollworm
N:Alternate names: Hez-AKH
C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C:Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C:Accession: A24244
R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridd
Biochem. Biophys. Res. Commun. 135, 622-628, 1986
A:Title: Isolation and primary structure of a peptide from the corpora cardiaca of He
A:Reference number: A24244; MUID:86186794; PMID:3964263
A:Accession: A24244
A:Molecule type: protein
A:Residues: 1-9 <JAF>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta
E:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 85.0%; Score 17; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 4 FTSSW 8

RESULT 2

hypothetical protein 38 - staphylococcus aureus phage phi PVL
T00172
C:Species: Staphylococcus aureus phage phi PVL
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: T00172
R:Kaneko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Y.
Bioescl. Biotechnol. Biochem. 61, 1960-1962, 1997
A:Title: Pantone-Valentine leukocidin genes in a phage-like particle isolated from mit
A:Reference number: Z14119; MUID:98067870; PMID:9404084
A:Accession: T00172
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-53 <KAN>
A:Cross-references: EMBL:AB009866; NID:d1204727; PIDN:BAA31912.1; PID:d1032873

Query Match 85.0%; Score 17; DB 2; Length 53;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 28 FTTAW 32

RESULT 3

D89989
 hypothetical protein SAS063 [imported] - *Staphylococcus aureus* (strain N315)
 C:Species: *Staphylococcus aureus*
 C:Date: 10-May-2001 #sequence-revision 10-May-2001 #text-change 22-Oct-2001
 C:Accession: D89989
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 L:ncet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: D89989
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-53 <KUR>
 A:Cross-references: GB:BA000018; PID:G13701784; PIDN:BA843077.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: SAS063

Query Match

Best Local Similarity 85.0%; Score 17; DB 2; Length 53;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 28 FTAW 32

RESULT 4

129202
 hypothetical protein F28F9.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence-revision 15-Oct-1999 #text-change 15-Oct-1999
 C:Accession: T29202
 R:Neelson, J.; Wohlmann, P.
 submitted to the EMBL Data Library, September 1996
 A:Description: The sequence of *C. elegans* cosmid F28F9.
 A:Reference number: 220587
 A:Accession: T29202
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-63 <NEU>
 A:Cross-references: EMBL:U70850; PIDN:AA09124.1; GSPDB:GN00022; CESP:F28F9.3
 A:Experimental source: strain Bristol N2; clone F28F9
 C:Genetics:
 A:Gene: CESP:F28F9.3
 A:Map position: 4
 A:Introns: 38/1

Query Match

Best Local Similarity 85.0%; Score 17; DB 2; Length 63;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 30 FATAW 34

RESULT 5

A32613
 adipokinetic hormone precursor - tobacco hornworm
 C:Species: *Manduca sexta* (tobacco hornworm)
 C:Date: 21-May-1990 #sequence-revision 21-May-1990 #text-change 18-Jun-1999
 C:Accession: A32613
 R:Bradfield, J.I.; Keeley, L.L.
 J. Biol. Chem. 264, 12791-12793, 1989
 A:Title: Adipokinetic hormone gene sequence from *Manduca sexta*.
 A:Reference number: A32613; MUID:89327232; PMID:2753887
 A:Accession: A32613
 A:Molecule type: DNA

A:Residues: 1-65 <RA>

A:Cross-references: GB:J04972; NID:G159478; PIDN:AAA29299.1; PID:G159479

C:Genetics:

A:Introns: #status absent

C:Superfamily: adipokinetic hormone

F:1-19/Domains: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamate

F:20-28/Product: adipokinetic hormone #status predicted <STG>

F:28/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

F:28/Modified site: amidated carboxyl end (Gly) (amide in mature form from following

Query Match

Best Local Similarity 85.0%; Score 17; DB 1; Length 65;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 23 FTSSW 27

RESULT 6

112860
 hypothetical protein yopZ - *Bacillus subtilis* phage SPBc2
 C:Species: *Bacillus subtilis* phage SPBc2
 C:Date: 13-Aug-1999 #sequence-revision 13-Aug-1999 #text-change 15-Oct-1999
 C:Accession: T12860; H69918
 R:Lazarevic, V.; Diesterhoeft, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.
 submitted to the EMBL Data Library, August 1997
 A:Description: The complete nucleotide sequence of the *Bacillus subtilis* SPBc2 pro
 A:Reference number: 217583
 A:Accession: T12860
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-67 <LAZ>
 A:Cross-references: EMBL:AF020713; NID:G3025478; PID:G3025574; PIDN:ANC13069.1
 R:Kunz, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Ber
 C: Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holstappel, S.; Hosono, S.; Hullo, M
 Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portele
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Sekiguchi, J.; Sekowska, A.; Se
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunori, K.; Yata, K.; Yoshida
 A:Authors: Yoshikawa, H.F.; Zumslein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: H69918
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-67 <KUN>
 A:Cross-references: GB:Z99114; GB:Z99115; GB:AL009126; NID:G2634478; PIDN:CAB13989.1;
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yopZ

Query Match

Best Local Similarity 85.0%; Score 17; DB 2; Length 67;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 49 FASSW 53

RESULT 7

A86942
 hypothetical protein [imported] - *Mycobacterium leprae*
 C:Species: *Mycobacterium leprae*

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: A86942
 R: Cole, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
 R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
 eam, M.A.; Rutherford, K.M.
 Nature 409, 1007-1011, 2001
 A: Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sc
 A: Title: Massive gene decay in the leprosy bacillus.
 A: Reference number: A86909; MUID:21128732; PMID:11234002
 A: Accession: A86942
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-70 <STO>
 A: Cross-references: GB:A1450380; NID:q13092599; PIDN:CAC29773.1; GSPDB:GN00147
 C: Genes:
 A: Gene: ML0265

Query Match 85.0%; Score 17; DB 2; Length 70;
 Best Local Similarity 40.0%; Pred. No. 1.5e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 Db 14 FTTSM 18

RESULT 8
 S15137
 Thioredoxin h2 - spinach (fragments)
 C: Species: Spinacia oleracea (spinach)
 C: Date: 25-Feb-1994 #sequence_revision 26-Jul-1996 #text_change 23-May-1997
 C: Accession: S15137
 R: Marcus, F.; Chamberlain, S.H.; Chu, C.; Maslarz, F.R.; Shin, S.; Yee, B.C.; Buchanan,
 Arch. Biochem. Biophys. 287, 195-198, 1991
 A: Title: Plant thioredoxin h: an animal-like thioredoxin occurring in multiple cell comp
 A: Reference number: S15137; MUID:91378382; PMID:1897969
 A: Accession: S15137
 A: Molecule type: protein
 A: Residues: 1-72 <MAR>
 C: Superfamily: thioredoxin; thioredoxin homology
 C: Keywords: redox-active disulfide

Query Match 85.0%; Score 17; DB 2; Length 72;
 Best Local Similarity 40.0%; Pred. No. 1.6e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 Db 6 FTASW 10

RESULT 9
 S18581
 pufo protein - Rhodobacter sphaeroides
 C: Species: Rhodobacter sphaeroides
 C: Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 13-Sep-1998
 C: Accession: S18581; S32854
 R: Hunter, C.N.; McEllyn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.
 Mol. Microbiol. 5, 2649-2661, 1991
 A: Title: DNA sequencing and complementation/deletion analysis of the bchA-puf operon reg
 A: Reference number: S18580; MUID:92140030; PMID:1779756
 A: Accession: S18581
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-77 <HUN>
 A: Cross-references: EMBL:X68795; NID:q49170; PID:q49175
 C: Genes:
 A: Gene: pufo
 C: Superfamily: pufo protein

Query Match 85.0%; Score 17; DB 2; Length 77;
 Best Local Similarity 40.0%; Pred. No. 1.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 Db 60 FASAW 64

RESULT 10
 T50756
 pufo protein [imported] - Rhodobacter sphaeroides
 C: Species: Rhodobacter sphaeroides
 C: Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
 C: Accession: T50756
 R: Choudhary, M.; Kaplan, S.
 Nucleic Acids Res. 28, 862-867, 2000
 A: Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroid
 A: Reference number: Z52222; MUID:20115911; PMID:10648776
 A: Accession: T50756
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: 1-77 <CHO>
 A: Cross-references: EMBL:AF195122; PIDN:AAF24300.1
 A: Experimental source: strain 2.4.1
 C: Genes:
 A: Gene: pufo
 C: Superfamily: pufo protein

Query Match 85.0%; Score 17; DB 2; Length 77;
 Best Local Similarity 40.0%; Pred. No. 1.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 Db 60 FASAW 64

RESULT 11
 F69268
 hypothetical protein AF0149 - Archaeoglobus fulgidus
 C: Species: Archaeoglobus fulgidus
 C: Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C: Accession: F69268
 R: Kleink, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
 A: Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A: Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A: Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
 A: Reference number: A69250; MUID:98049343; PMID:9389475
 A: Accession: F69268
 A: Status: preliminary; nucleic acid sequence not shown; translation not shown
 A: Molecule type: DNA
 A: Residues: 1-84 <KLE>
 A: Cross-references: GB:AE001096; GB:AE000782; NID:92689419; PIDN:AA91088.1; PID:9265

Query Match 85.0%; Score 17; DB 2; Length 84;
 Best Local Similarity 40.0%; Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 Db 42 FAAMW 46

RESULT 12
 B46264
 thioredoxin 2 - slime mold (Dictyostellium discoideum) (fragment)
 C: Species: Dictyostellium discoideum
 C: Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 11-Jun-1999
 C: Accession: B46264
 R: Welterauer, B.; Jacquot, J.P.; Veron, M.
 J. Biol. Chem. 267, 9895-9904, 1992
 A: Title: Thioredoxins from Dictyostellium discoideum are a developmentally regulated m

A:Reference number: A46264; MUID:92250653; PMID:1577820
 A:Accession: B46264
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-88 <MEY>
 A:Cross-references: GB:M91382; NID:q167930; PIDN:AAA33259.1; PID:q167931
 C:Superfamily: Thiorodoxin; Thiorodoxin homology
 I:8-88/Domain: Thiorodoxin homology <THR>

Query Match
 Best Local Similarity 85.0%; Score 17; DB 2; Length 88;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 1 FXXXW 5
 DB 26 FSSTW 30

RESULT 13

F47624

1g heavy chain V-I region - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C:Accession: F47624

R:Haite, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
 J. Exp. Med. 171: 1721-1737, 1990

A:Title: Eleven distinct V-H gene families and additional patterns of sequence variation
 A:Reference number: A47624; MUID:90237760; PMID:2110243
 A:Accession: F47624

A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA

A:Residues: 1-98 <HAI>

C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: Immunoglobulin homology <IMV>

Query Match

Best Local Similarity 85.0%; Score 17; DB 2; Length 98;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 1 FXXXW 5
 DB 29 FSSTW 33

RESULT 14

S37447

gene E2 protein - human papillomavirus type 5 (fragment)
 C:Species: human papillomavirus type 5
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999

C:Accession: S37447

R:Deau, A.C.

submitted to the EMBL Data Library, August 1993
 A:Reference number: S37440

A:Accession: S37447

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-99 <DEA>

A:Cross-references: EMBL:X74651; NID:q404204; PIDN:CAA52715.1; PID:q404205
 C:Superfamily: papillomavirus E2 protein

Query Match

Best Local Similarity 85.0%; Score 17; DB 2; Length 99;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 1 FXXXW 5
 DB 46 FSSTW 50

RESULT 15

S37448

gene E2 protein - human papillomavirus type 5 (fragment)
 C:Species: human papillomavirus type 5 (fragment)

C:Species: human papillomavirus type 5
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 12-Apr-1995
 C:Accession: S37448

R:Deau, A.C.

submitted to the EMBL Data Library, August 1993
 A:Reference number: S37440

A:Accession: S37448

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-99 <DEA>

A:Cross-references: EMBL:X74652
 C:Superfamily: papillomavirus E2 protein

Query Match

Best Local Similarity 85.0%; Score 17; DB 2; Length 99;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 1 FXXXW 5
 DB 46 FSSTW 50

Search completed: January 29, 2003, 14:12:36
 Job time : 16 secs

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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:07:27 ; Search time 11 Seconds
(without alignments)
18.853 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	17	85.0	38	PSAI_PROMA	O87786 prochloroco
2	17	85.0	65	AKH_MANSE	P08901 manduca sex
3	17	85.0	77	PUPF_RHOSE	P16069 rhodopacter
4	17	85.0	84	Y149_ARCFU	O30088 archaeoglob
5	17	85.0	88	TH12_DICDI	P29446 dictyostell
6	17	85.0	93	CD06_HUMAN	O99440 homo sapien
7	17	85.0	104	TH10_BOVIN	O97680 bos taurus
8	17	85.0	104	TH10_CALJA	O9bdj3 callithrix
9	17	85.0	104	TH10_CHICK	P08629 gallus gall
10	17	85.0	104	TH10_HORSE	O97508 equus caball
11	17	85.0	104	TH10_HUMAN	P10759 homo sapien
12	17	85.0	104	TH10_MACMU	P29451 macaca mula
13	17	85.0	104	TH10_MOUSE	P10639 mus musculu
14	17	85.0	104	TH10_OPNHA	O98tx1 ophiophagus
15	17	85.0	104	TH10_PIG	P82460 sus scrofa
16	17	85.0	104	TH10_RABIT	P08628 oryctolagus
17	17	85.0	104	TH10_SHEEP	P11232 rattus norv
18	17	85.0	104	TH10_SHEEP	P50413 ovis aries
19	17	85.0	107	TH10_ICTRU	O9dql3 ictalurins p
20	17	85.0	112	TH11_ARATH	P80028 chlamydomon
21	17	85.0	114	TH11_ARATH	P29448 arabidopsis
22	17	85.0	115	TH11_FAGES	P01780 homo sapien
23	17	85.0	116	TH11_FAGES	O96419 fagopyrum e
24	17	85.0	118	TH12_TOBAC	O07050 nicotiana t
25	17	85.0	118	TH12_TOBAC	O42403 arabidopsis
26	17	85.0	118	TH15_ARATH	O39241 arabidopsis
27	17	85.0	118	TH1H_RICCO	O43636 ricinus com
28	17	85.0	119	TH12_BRANA	O39239 arabidopsis
29	17	85.0	119	TH14_ARATH	O42443 oryza sativ
30	17	85.0	122	TH1H_ORYSA	O65049 picea maria
31	17	85.0	125	TH1H_PICMA	P29449 piceoliana t
32	17	85.0	126	TH1H_TOBAC	O64394 trifolium ae
33	17	85.0	126	TH1H_WHEAT	

34	17	85.0	133	1	TH12_ARATH	O38879 arabidopsis
35	17	85.0	141	1	YE17_YEAST	P40102 saccharomyc
36	17	85.0	174	1	YC21_PORPU	P51380 porphyra pu
37	17	85.0	182	1	FCPD_MACPY	O40298 macrocystis
38	17	85.0	208	1	ENGB_HELPJ	O9z142 hellicobacte
39	17	85.0	208	1	ENGB_HELPY	O26087 hellicobacte
40	17	85.0	211	1	FCPF_MACPY	O40300 macrocystis
41	17	85.0	212	1	HAG2_EIKCO	P35648 eikenella c
42	17	85.0	216	1	FCPC_MACPY	O40299 macrocystis
43	17	85.0	232	1	HXB9_XENILA	P31272 xenopus lae
44	17	85.0	241	1	PCPB_HAEIN	P44570 haemophilus
45	17	85.0	251	1	GUNX_PRUPE	P38534 prunus pers

ALIGNMENTS

RESULT 1

PSAI_PROMA

STANDARD:

PRT: 38 AA.

AC O87786;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Photosystem I reaction center subunit VIII.

GN PSAI.
OS Prochlorococcus marinus.
OC Bacteria: Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1219;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=SAAG / CCMP 1375;
RA van der Staay G.W.M., Moon-Van Der Staay S.Y., Garczarek L.,
RA Partensky F.;
RT "Characterization of the photosystem I subunits Psai and Psal from two
RT strains of the marine cyanobacterium P. marinus";
RL Photosyn. Res. 57:183-191(1998).
CC -!- FUNCTION: MAY HELP IN THE ORGANIZATION OF THE PSAI SUBUNIT.
CC -!- SIMILARITY: BELONGS TO THE PSAI FAMILY.

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DR EMBL: Z98594; CAB1178.1; ALT_INIT.
DR InterPro: IPR001302; PSI_8.
DR Pfam: PF00796; PSI_8; 1.
KW Photosystem I; Photosynthesis; Transmembrane.
KW TRANSMEM
FT 12 32
FT 38 AA; 4081 MW; 19DECDAB650A2F2 CRC64;
SQ SEQUENCE

Query Match 85.0%; Score 17; DB 1; Length 38;
Best Local Similarity 40.0%; Pred. No. 4.6e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 FXXXW 5
Db 5 FAATW 9

RESULT 2
ID AKH_MANSE STANDARD: PRT: 65 AA.

AC P08901;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Adipokinetic hormone precursor (AKH).


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Db      60 FASAW 64

RESULT 4
Y149_ARCFU STANDARD: PRT: 84 AA.
ID Y149_ARCFU
AC O30088:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AF0149.
OS Archaeoglobus fulgidus.
OC Archaea: Euryarchaeota: Archaeoglobi: Archaeoglobales:
OC Archaeoglobaceae: Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwin M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriades N.C., Gill S.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC -----
DR EMBL: AE001096; AAB91088.1; -.
DR TIGR: AF0149; -.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 4 20 POTENTIAL.
FT TRANSMEM 27 49 POTENTIAL.
FT TRANSMEM 59 81 POTENTIAL.
SQ SEQUENCE 84 AA; 8893 MW; E2PDLFCGFEBFLEE CXC64;
Query Match 85.0%; Score 17; DB 1; Length 84;
Best Local Similarity 40.0%; Pred. No. 8,4e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0
Oy 1 FXXW 5
Db 42 FAAMW 46

RESULT 5
TH12_DICD1 STANDARD: PRT: 88 AA.
ID TH12_DICD1
AC P29446;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thiorodoxin 2 (Fragment).
GN TRX2 OR TRX2.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota: Mycetozoa: Dictyostellida: Dictyostellum.

```

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OX NCB1_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92250653; PubMed=1577820;
RA Wetleauer B., Jacquot J.-P., Veron M.;
RT "thioredoxins from Dictyostelium discoideum are a developmentally
RT regulated multigene family."
RL J. Biol. Chem. 267:9895-9904(1992).
CC -!- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -----
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CC -----
DR EMBL: M91382; AAA33259.1; -.
DR PIR: B46264; B46264.
DR HSPSP: P10599; 1ERV.
DR DickeyDB: DD05030; trxB.
DR InterPro: IPR00085; ThioRed.
DR Pfam: PF00085; ThioRed.1.
DR PROSITE: PS00194; THIOREDOXIN_1.
KW Redox-active center; Electron transport; Multigene family.
FT DISULFID 31 34 REDOX-ACTIVE (BY SIMILARITY).
FT NON_TER 88 88
SQ SEQUENCE 88 AA; 10102 MW; CEC73BCEFACB607C CRC64;
OY 1 FXXXXX 5
DY 26 FSAAW 30

RESULT 6
CD06_HUMAN STANDARD; PRT; 93 AA.
ID CD06_HUMAN
AC Q99440;
PT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein C4orf6 (AC1 protein).
GN C4ORF6 OR AC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97169148; PubMed=9016955;
RA Kito K., Ito T., Sakaki Y.;
RT "Fluorescent differential display analysis of gene expression in
RT differentiating neuroblastoma cells."
RL Gene 184:73-81(1997).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEUROBLASTOMA.
CC -----
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CC -----
DR EMBL: D82070; BAA11534.1; -.
DR GeneV; HGNC:13716; C4orf6.

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SQ SEQUENCE 93 AA: 10499 MW: A8786ACAA990215 CRC64:
 Query Match
 Best Local Similarity 85.0%; Score 17; DB 1; Length 93;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 DB 69 FAASW 73

RESULT 7
 THIO_BOVIN STANDARD; PRT; 104 AA.
 AC 097680;
 CT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Thioresoxin.
 GN TXN.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;
 CC Bovidae; Bovineae; Bos.
 CX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20189621; PubMed=10727087;
 RA Terashima H., Goloh S., Yagi K., Mizoguchi T.;
 RT "cDNA sequence of bovine thioresoxin";
 RL DNA Seq. 10:331-333(1999).
 CC -!- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF104105; AAC83380.1;
 DR HSSP; P10599; 1ERT.
 DR InterPro: IPR000063; Thiores.
 DR Pfam: PF00085; thioresd.1.
 DR PRINTS: PRO0421; THIOREDOXIN.
 DR PROSITE: PS00194; THIOREDOXIN.1.
 KW Redox-active center; Electron transport.
 FT INT_MET 0
 FT DISULFID 31 34 BY SIMILARITY.
 FT SEQUENCE 104 AA; 11681 MW; 506CF9696A2208D CRC64;
 SO

Query Match
 Best Local Similarity 85.0%; Score 17; DB 1; Length 104;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 DB 26 FSATW 30

RESULT 8
 THIO_CALJA STANDARD; PRT; 104 AA.
 AC 09BD03;
 CT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Thioresoxin.
 GN TXN.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;
 CC Bovidae; Bovineae; Bos.
 CX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20189621; PubMed=10727087;
 RA Terashima H., Goloh S., Yagi K., Mizoguchi T.;
 RT "cDNA sequence of bovine thioresoxin";
 RL DNA Seq. 10:331-333(1999).
 CC -!- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF104105; AAC83380.1;
 DR HSSP; P10599; 1ERT.
 DR InterPro: IPR000063; Thiores.
 DR Pfam: PF00085; thioresd.1.
 DR PRINTS: PRO0421; THIOREDOXIN.
 DR PROSITE: PS00194; THIOREDOXIN.1.
 KW Redox-active center; Electron transport.
 FT INT_MET 0
 FT DISULFID 31 34 BY SIMILARITY.
 FT SEQUENCE 104 AA; 11681 MW; 506CF9696A2208D CRC64;
 SO

Query Match
 Best Local Similarity 85.0%; Score 17; DB 1; Length 104;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 DB 26 FSATW 30

RESULT 9
 THIO_CHICK STANDARD; PRT; 104 AA.
 AC P08629;
 CT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DE Thioresoxin.
 GN TXN.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88257080; PubMed=2838473;
 RA Jones S.W., Luk K.-C.;
 RT "Isolation of a chicken thioresoxin cDNA clone. Thioresoxin mRNA is
 RT differentially expressed in normal and Rous sarcoma virus-transformed
 RT chicken embryo fibroblasts";
 RL J. Biol. Chem. 263:9607-9611(1988).
 CC -!- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide

DE Thioresoxin.
 GN TXN OR TRX.
 OS Gallitrix jacchus (Common marmoset).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
 CC Callitrix.
 CX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21576430; PubMed=11719593;
 RA Lopata A., Sibson M.C., Enders A.C., Bloomfield K.L., Gregory M.S.,
 RA Trapani G.D., Perkins A.V., Tomlison K.F., Clarke F.M.;
 RT "Expression and localization of thioresoxin during early implantation
 RT in the marmoset monkey";
 RL Mol. Hum. Reprod. 7:1159-1165(2001).
 CC -!- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions.
 CC -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF353204; AAK30295.1;
 DR HSSP; P10599; 1ERT.
 DR InterPro: IPR000063; Thiores.
 DR Pfam: PF00085; thioresd.1.
 DR PRINTS: PRO0421; THIOREDOXIN.
 DR PROSITE: PS00194; THIOREDOXIN.1.
 KW Redox-active center; Electron transport.
 FT INT_MET 0
 FT DISULFID 31 34 BY SIMILARITY.
 FT SEQUENCE 104 AA; 11626 MW; 3E0F524A04B8E81 CRC64;
 SO

Query Match
 Best Local Similarity 85.0%; Score 17; DB 1; Length 104;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 DB 26 FSATW 30

RESULT 9
 THIO_CHICK STANDARD; PRT; 104 AA.
 AC P08629;
 CT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DE Thioresoxin.
 GN TXN.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88257080; PubMed=2838473;
 RA Jones S.W., Luk K.-C.;
 RT "Isolation of a chicken thioresoxin cDNA clone. Thioresoxin mRNA is
 RT differentially expressed in normal and Rous sarcoma virus-transformed
 RT chicken embryo fibroblasts";
 RL J. Biol. Chem. 263:9607-9611(1988).
 CC -!- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide

CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -I- SIMILARITY: BELONGS TO THE THIOREDoxIN FAMILY.
CC -----
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CC -----
DR EMBL: J03882; AAA9092.1; -
DR PIR: A30006; A30006.
DR HSSP: P10599; 1ERR.
DR InterPro: IPR000063; ThioRed.
DR Pfam: PF00085; ThioRed; 1.
DR PRINTS: PR00421; THIOREDoxIN.
DR PROSITE: PS00194; THIOREDoxIN; 1.
KW Redox-active center; Electron transport.
FT INIT_MET 0 BY SIMILARITY.
FT DISULFID 31 34 REDOX-ACTIVE (BY SIMILARITY).
SQ SEQUENCE 104 AA; 11569 MW; 60B6B759010BB12 CRC64;
Query Match 85.0%; Score 17; DB 1; Length 104;
Best Local Similarity 40.0%; Pred. No. 9.9e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 FXXXW 5
DB 26 FSATW 30
RESULT 10
THIO_HUMAN
ID THIO_HUMAN STANDARD; PRT; 104 AA.
AC 097508;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thioredoxin.
GN TXN.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Thoroughbred;
RA Tajima Y., Ishida N.;
RT "Molecular cloning of equine thioredoxin.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -I- SIMILARITY: BELONGS TO THE THIOREDoxIN FAMILY.
CC -----
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CC -----
DR EMBL: AB022431; BAA37154.1; -
DR HSSP: P10599; 1ERV.
DR InterPro: IPR000063; ThioRed.
DR Pfam: PF00085; ThioRed; 1.
DR PRINTS: PR00421; THIOREDoxIN.
DR PROSITE: PS00194; THIOREDoxIN; 1.

KW Redox-active center; Electron transport.
FT INIT_MET 0 BY SIMILARITY.
FT DISULFID 31 34 REDOX-ACTIVE (BY SIMILARITY).
SQ SEQUENCE 104 AA; 11605 MW; 5E6C1092964C206D CRC64;
Query Match 85.0%; Score 17; DB 1; Length 104;
Best Local Similarity 40.0%; Pred. No. 9.9e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 FXXXW 5
DB 26 FSATW 30
RESULT 11
THIO_HUMAN
ID THIO_HUMAN STANDARD; PRT; 104 AA.
AC P10599; 096K13;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thioredoxin (ATL-derived factor) (ADF) (Surface associated sulphhydryl
DE protein) (SASP).
GN TXN OR TRDX OR TRX OR TRX1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91340156; PubMed=1874447;
RA Tonissen K.F., Wells J.R.E.;
RT "Isolation and characterization of human thioredoxin-encoding genes.";
RL Gene 102:221-228(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89008454; PubMed=3170595;
RA Wollman E.E., D'Aurion L., Rimskey L., Shaw A., Jacquot J.-P.,
RA Wingfield P., Graber P., Dessarps F.;
RT "Cloning and expression of a cDNA for human thioredoxin.";
RL J. Biol. Chem. 263:15506-15512(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89251607; PubMed=2785919;
RA Tagaya Y., Maeda K.-I., Mitsui A., Kudo N., Matsui H., Hamuro J.,
RA Brown N., Arai K.-I., Yokota T., Wakasugi H., Yodoi J.;
RT "ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to
RT thioredoxin: possible involvement of dithiol-reduction in the IL-2
RT receptor induction.";
RL EMBO J. 8:757-764(1989).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RA Reddy P.G., Bhuyan D.K., Bhuyan K.C.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RA Liu A., Lou M.F.;
RT "Cloning, purification and characterization of human lens
RT thioredoxin.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Xu J.Y., Xu L., Li K.S., Dai R.;
RT "Cloning and sequencing of thioredoxin cDNA from human brain.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

[8]
 RE- SEQUENCE OF 1-14.
 RX MEDLINE=91151337; PubMed=1998498;
 RA Martin H., Dean M.;
 RT "Identification of a thioredoxin-related protein associated with
 R1 plasma membranes.";
 RL Biochem. Biophys. Res. Commun. 175:123-128(1991).
 RN [9]
 RE STRUCTURE BY NMR.
 RX MEDLINE=90057393; PubMed=2684271;
 RA Forman-Kay J.D., Clore G.M., Driscoll P.C., Wingfield P.,
 RA Richards F.M., Gronenborn A.M.;
 RT "A proton nuclear magnetic resonance assignment and secondary
 RT structure determination of recombinant human thioredoxin.";
 RL Biochemistry 28:7088-7097(1989).
 RN [10]
 RE STRUCTURE BY NMR.
 RX MEDLINE=91159399; PubMed=2001356;
 RA Forman-Kay J.D., Clore G.M., Wingfield P., Gronenborn A.M.;
 RT "High-resolution three-dimensional structure of reduced recombinant
 RT human thioredoxin in solution.";
 RL Biochemistry 30:2685-2698(1991).
 RN [11]
 RE STRUCTURE BY NMR.
 RX MEDLINE=95006318; PubMed=7922028;
 RA Qin J., Clore G.M., Gronenborn A.M.;
 RT "The high-resolution three-dimensional solution structures of the
 RT oxidized and reduced states of human thioredoxin.";
 RL Structure 2:503-522(1994).
 RN [12]
 RE STRUCTURE BY NMR.
 RX MEDLINE=96347359; PubMed=8736558;
 RA Qin J., Clore G.M., Kennedy W.P., Kuszewski J., Gronenborn A.M.;
 RT "The solution structure of human thioredoxin complexed with its
 RT target from Ref-1 reveals peptide chain reversal.";
 RL Structure 4:613-620(1996).
 RN [13]
 RE X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
 RX MEDLINE=96399719; PubMed=8805557;
 RA Weichsel A., Gasdaska J.R., Powis G., Montfort W.R.;
 RT "Crystal structures of reduced, oxidized, and mutated human
 RT thioredoxins: evidence for a regulatory homodimer.";
 RL Structure 4:735-751(1996).
 RN [14]
 RE X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF MUTANT ASN-60.
 RX MEDLINE=98039128; PubMed=9369469;
 RA Andersen J.F., Sanders D.A., Gasdaska J.R., Weichsel A., Powis G.,
 RA Montfort W.R.;
 RT "Human thioredoxin homodimers: regulation by pH, role of aspartate
 RT 60, and crystal structure of the aspartate 60 --> asparagine
 RT mutant.";
 RL Biochemistry 36:13979-13988(1997).
 RN [15]
 RE ACTIVITY.
 RX MEDLINE=91097576; PubMed=2176490;
 RA Jaquot J.-P., de Lamotte F., Fontecay M., Scherrenmann P.,
 RA Decollignies P., Migoniac-Maslow M., Wollman E.;
 RT "Human thioredoxin reactivity-structure/function relationship.";
 RL Biochem. Biophys. Res. Commun. 173:1375-1381(1990).
 CC -1- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions.
 CC -1- FUNCTION: ADF AUGMENTS THE EXPRESSION OF THE INTERLEUKIN-2
 CC RECEPTOR TAC (IL2R/P55).
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE THIOREDOKIN FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X77594; CAA54687.1; -;
 DR EMBL: X54539; CAA38410.1; -;
 DR EMBL: X54540; CAA38410.1; JOINED.
 DR EMBL: X54541; CAA38410.1; JOINED.
 DR EMBL: J04026; AAA74596.1; -;
 DR EMBL: AE276919; AAF86466.1; -;
 DR EMBL: AY004872; AAF87085.1; -;
 DR EMBL: AF313911; AAG34699.1; -;
 DR EMBL: BC003377; AAH03377.1; -;
 DR PIR: A31993; A31993.
 DR PIR: S04106; S04106.
 DR PIR: JH0568; JH0568.
 DR PDB: 1TRX; 15-JAN-93.
 DR PDB: 1TRS; 30-SEP-94.
 DR PDB: 1TRU; 30-SEP-94.
 DR PDB: 1TRV; 30-SEP-94.
 DR PDB: 1A1U; 07-JUL-97.
 DR PDB: 1ERT; 14-OCT-96.
 DR PDB: 1ERU; 01-AUG-96.
 DR PDB: 1ERV; 14-OCT-96.
 DR PDB: 1ERW; 14-OCT-96.
 DR PDB: 1C0G; 01-AUG-96.
 DR PDB: 1C0H; 01-AUG-96.
 DR PDB: 1MDI; 03-JUN-95.
 DR PDB: 1MDJ; 20-JUL-95.
 DR PDB: 1MDK; 20-JUL-95.
 DR PDB: 1AUC; 25-FEB-98.
 DR SWISS-2DPAGE: P10599; HUMAN.
 DR Aatrus/Ghent-2DPAGE; 8006; IEF.
 DR PHCI-2DPAGE; P10599; -;
 DR Sienna-2DPAGE; P10599; -;
 DR Genew; HGNC:12435; TXN.
 DR MIM: 187700; -;
 DR InterPro: IPR00063; ThioRed.
 DR Pfam: PF00085; ThioRed; 1.
 DR PRINTS: PR00421; THIOREDOKIN.
 DR PROSITE: PS00194; THIOREDOKIN; 1.
 KW Redox-active center; Electron transport; 3D-structure.
 FT INIT MET 0
 FT DISULFID 31 34 REDOX-ACTIVE.
 FT DISULFID 72 72 INTERCHAIN.
 FT CONFLICT 38 38 K -> N (IN REF. 2 AND 4).
 FT CONFLICT 73 73 M -> T (IN REF. 2 AND 4).
 FT STRAND 2 3
 FT HELIX 7 16
 FT TURN 18 19
 FT STRAND 22 27
 FT HELIX 32 35
 FT TURN 36 37
 FT TURN 38 41
 FT HELIX 42 43
 FT TURN 44 47
 FT STRAND 52 57
 FT TURN 56 60
 FT HELIX 62 68
 FT TURN 69 69
 FT STRAND 75 80
 FT TURN 81 82
 FT STRAND 83 89
 FT HELIX 94 103
 SQ SEQUENCE 104 AA; 11606 MW; 7FFABDF3B6BE833A CRC64;
 Query Match 85.0%; Score 17; DB 1; Length 104;
 Best Local Similarity 40.0%; Pred. No. 9,9e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FXXW 5
 1 1

Db 26 FSATW 30

RESULT 12
THIO_MACMU STANDARD; PRT: 104 AA.

AC P29451:
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thioedoxin.
GN TXN.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92181438; PubMed=1543487;
RA An G., Wu R.;
RT Thioedoxin gene expression is transcriptionally up-regulated by
RT retinol in monkey conducting airway epithelial cells.";
RL Biochem. Biophys. Res. Commun. 183:170-175(1992).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M84643; AAA36921.1; -
DR PIR: J50667; J50667.
DR HSSP: P10599; 1ERT.
DR InterPro: IPR000063; ThioRed.
DR Pfam: PF00085; ThioRed.
DR PRINTS: PR00421; ThioREDOXIN.
DR PROSITE: PS00194; THIOREDOXIN; 1.
KW Redox-active center; Electron transport.
FT INIT_MET 0 BY SIMILARITY.
FT DISULFID 31 34 REDOX-ACTIVE (BY SIMILARITY).
SQ SEQUENCE 104 AA; 11606 MW; C804D5152F8870EB CRC64;

Query Match 85.0%; Score 17; DB 1; Length 104;
Best Local Similarity 40.0%; Pred. No. 9.9e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 26 FSATW 30

RESULT 13
THIO_MOUSE STANDARD; PRT: 104 AA.

AC P10639; Q9D8R0;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thioedoxin (ATL-derived factor) (ADF).
GN TXN OR TXN1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=89251607; PubMed=2785919;
RA Tagaya Y., Maeda Y., Mitsu A., Kudo N., Matsui H., Hamuro J.,
RA Brown N., Arai K.-I., Yokota T., Wakasugi H., Yodoi J.;
RT "ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to
RT thioedoxin: possible involvement of dithiol-reduction in the IL-2
RT receptor induction.";
RL EMBO J. 8:757-764(1989).
RN [2]
RN REVISIONS.
RX MEDLINE=94244626; PubMed=8187776;
RA Tagaya Y., Maeda Y., Mitsu A., Kudo N., Matsui H., Hamuro J.,
RA Brown N., Arai K.-I., Yokota T., Wakasugi H., Yodoi J.;
RL EMBO J. 13:2244-2244(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX SRAIN=129/SV; TISSUE=Liver;
RX MEDLINE=95137382; PubMed=7835695;
RA Matsui M., Taniguchi Y., Hirota K., Taketo M., Yodoi J.;
RT "Structure of the mouse thioedoxin-encoding gene and its processed
RT pseudogene.";
RL Gene 152:165-171(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX SRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Ando S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fledschman W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -1- FUNCTION: ADF AUGMENTS THE EXPRESSION OF THE INTERLEUKIN-2
CC RECEPTOR TAC (IL2R/P55).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X77585; CA454688.1; -
DR EMBL: D21859; BAA04881.1; -
DR EMBL: D21855; BAA04881.1; JOINED.
DR EMBL: D21856; BAA04881.1; JOINED.
DR EMBL: D21857; BAA04881.1; JOINED.
DR EMBL: D21858; BAA04881.1; JOINED.

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DR EMBL: AK007537; BAB25096.1; -
DR EMBL: AK007790; BAB25256.1; -
DR EMBL: BC010756; AAH10756.1; -
DR PIR: S04107; S04107.
DR HSSP: P10599; 1ERT.
DR SWISS-2DPAGE: P10639; MOUSE.
DR MGD: MGI:98874; Txn1.
DR InterPro: IPR000063; ThioRed.
DR Pfam: PF00085; ThioRed; 1.
DR PRINTS: PR00421; THIOREDOXIN.
DR PROSITE: PS00194; THIOREDOXIN; 1.
DR Redox-active center; Electron transport.
FW INT_MET 0
FW DISULFID 31 34 REDOX-ACTIVE (BY SIMILARITY).
FW CONFLICT 99 99 S->C (IN REF. 4; BAB25256).
SQ SEQUENCE 104 AA; 11544 MW; 60BE6196090AC773 CRC64;

Query Match 85.0%; Score 17; DB 1; Length 104;
Best Local Similarity 40.0%; Pred. No. 9.9e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 26 FSATW 30

RESULT 14
THIO_OPNHA STANDARD; PRT; 104 AA.
AC Q98TXL;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thioredoxin.
GN TXN.
OS Ophiophagus hannah (King cobra) (Naja hannah).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Elapidae; Squamata; Scleroglossa; Serpentes; Colubridae;
OC NCB1_TaxID=8665;
ON [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Lee W., Liu H., Zhang Y.;
RT "cDNA sequence of Ophiophagus hannah venom gland thioredoxin
protein."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
CC -----
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CC -----
DR EMBL: AF321769; AAK09384.1; -
DR HSSP: P10599; 1ERT.
DR InterPro: IPR000063; ThioRed.
DR Pfam: PF00085; ThioRed; 1.
DR PRINTS: PR00421; THIOREDOXIN.
DR PROSITE: PS00194; THIOREDOXIN; 1.
DR Redox-active center; Electron transport.
FW INT_MET 0
FW DISULFID 31 34 REDOX-ACTIVE (BY SIMILARITY).
FW CONFLICT 99 99 S->C (IN REF. 4; BAB25256).
SQ SEQUENCE 104 AA; 11872 MW; 852B96C8EF850A7B CRC64;

Query Match 85.0%; Score 17; DB 1; Length 104;
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Best Local Similarity 40.0%; Pred. No. 9.9e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 26 FSATW 30

RESULT 15
THIO_PIG STANDARD; PRT; 104 AA.
AC P82460; Q95JF9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thioredoxin.
GN TXN.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
ON NCB1_TaxID=9823;
ON [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Yu G.W., Xu J.Y., Xu L., Cheung P.Y., Lee K.S.;
RT "The cloning and expression of porcine thioredoxin in E. coli."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-33.
RC TISSUE=Erythrocyte;
RA Lee K.S., Tang W.K., Cheung P.Y., Siu Y.L., Wong N.S.;
RL Submitted (MAY-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- TISSUE SPECIFICITY: ERYTHROCYTE.
CC -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
CC -----
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CC -----
DR EMBL: AF382821; AAK60272.1; -
DR HSSP: P10599; 1ERV.
DR InterPro: IPR000063; ThioRed.
DR Pfam: PF00085; ThioRed; 1.
DR PROSITE: PS00194; THIOREDOXIN; 1.
DR Redox-active center; Electron transport.
FW INT_MET 0
FW DISULFID 31 34 REDOX-ACTIVE (BY SIMILARITY).
FW CONFLICT 99 99 S->C (IN REF. 4; BAB25256).
SQ SEQUENCE 104 AA; 11697 MW; 9B16FF9696A2396A CRC64;

Query Match 85.0%; Score 17; DB 1; Length 104;
Best Local Similarity 40.0%; Pred. No. 9.9e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 26 FSATW 30

Search completed: January 29, 2003, 14:11:37
Job time : 11 secs
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:09:57 ; Search time 29 Seconds
(without alignments)
35.525 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL.21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_fodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioph:*
17: sp_archaeop.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	85.0	13	09XLI2	09XLI2 Bemisia tab
2	17	85.0	26	10 09S880	09S880 spinacia ol
3	17	85.0	32	2 005602	005602 pseudomonas
4	17	85.0	36	13 09PV61	09PV61 mola mola (
5	17	85.0	38	13 09PV63	09PV63 pseudopleur
6	17	85.0	40	13 09PV89	09PV89 triakis sp.
7	17	85.0	40	13 09PV88	09PV88 torpeda cal
8	17	85.0	40	13 09PV85	09PV85 osteoglossu
9	17	85.0	40	13 09PV84	09PV84 anguilla sp
10	17	85.0	40	13 09PV82	09PV82 barbatus tetr
11	17	85.0	40	13 09PV81	09PV81 esox lucius
12	17	85.0	40	13 09PV80	09PV80 pleuroglossu
13	17	85.0	40	13 09PV79	09PV79 galaxias ma
14	17	85.0	40	13 09PV78	09PV78 lampiris sp.
15	17	85.0	40	13 09PV77	09PV77 mugil cepha
16	17	85.0	40	13 09PV76	09PV76 hemiramphus

17	17	85.0	40	13 09PV77	09PV77 mugil cepha
18	17	85.0	40	13 09PV05	09PV05 hemiramphus
19	17	85.0	40	13 09PV04	09PV04 fundulus he
20	17	85.0	40	13 09PV75	09PV75 poecilia la
21	17	85.0	40	13 09PV03	09PV03 sargocentro
22	17	85.0	40	13 09PV02	09PV02 zeus faber
23	17	85.0	40	13 09PV74	09PV74 hippocampus
24	17	85.0	40	13 09PV73	09PV73 mastacembi
25	17	85.0	40	13 09PV01	09PV01 dendrochiru
26	17	85.0	40	13 09PV72	09PV72 lates calca
27	17	85.0	40	13 09PV00	09PV00 dicentrarch
28	17	85.0	40	13 09PV71	09PV71 epinephelus
29	17	85.0	40	13 09PV70	09PV70 mulius sp.
30	17	85.0	40	13 09PV78	09PV78 disostichu
31	17	85.0	40	13 09PV28	09PV28 salarias sp
32	17	85.0	40	13 09PV69	09PV69 cryptocentr
33	17	85.0	40	13 09PV68	09PV68 acanthurus
34	17	85.0	40	13 09PV66	09PV66 stromateus
35	17	85.0	40	13 09PV65	09PV65 colisa lail
36	17	85.0	40	13 09PV64	09PV64 channa sp.
37	17	85.0	40	13 09PV62	09PV62 ostracion s
38	17	85.0	40	13 09PV02	09PV02 polypterus
39	17	85.0	44	16 08XPJ4	08XPJ4 raietonia s
40	17	85.0	53	9 080077	080077 staphylococ
41	17	85.0	53	9 09B0G7	09B0G7 staphylococ
42	17	85.0	53	9 09G031	09G031 bacterioph
43	17	85.0	53	9 08SDM7	08SDM7 staphylococ
44	17	85.0	53	16 09S802	09S802 staphylococ
45	17	85.0	53	16 0931J8	0931J8 staphylococ

ALIGNMENTS

RESULT 1

09XLI2 ID 09XLI2 PRELIMINARY: PRT: 13 AA.
AC 01-NOV-1999 (TREMUREL. 12, Created)
DT 01-NOV-1999 (TREMUREL. 12, Last sequence update)
DT 01-NOV-2002 (TREMUREL. 21, Last annotation update)
DE Cytochrome oxidase I (Fragment).
OS Bemisia tabaci (Sweetpotato whitefly).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
OC Aleyrodiformes; Aleyrodidae; Aleyrodinae; Bemisia.
OX NCBI_TaxID=7058;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10583831;
RA Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,
RT "A phylogeographical analysis of the Bemisia tabaci species complex
based on mitochondrial DNA markers."
RL Mol. Ecol. 8:1683-1691(1999).
DR EMBL: AF10703; AAD28415.1; --
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 13 AA: 1639 MW: 8DD68729F5744365 CRC64;

Query Match Score 17: DB 8; Length 13:
Best local Similarity 40.0%; Pred. No. 8.2e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 3 FTSSW 7

RESULT 2
09S880 ID 09S880 PRELIMINARY: PRT: 26 AA.

AC Q9S880: 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE Thiorodoxin H2 (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 CX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.

3X MEDLINE=91378382; PubMed=1897989;
 3A Marcus F., Chamberlain S.H., Chu C., Maslarz F.R., Shin S., Yee B.C.,
 3B Buchanan B.B.;
 RT "Plant thiorodoxin h: an animal-like thiorodoxin occurring in multiple
 cell compartments.";
 RL Arch. Biochem. Biophys. 287:195-198(1991).
 DR InterPro: IPR000063; Thiorod.
 DR Pfam: PF00085; Thiorod. 1.
 DR PROSITE: PS00194; THIOREDOXIN; 1.
 KW Redox-active center.
 IT NON_TER 1
 IT NON_TER 1
 SO SEQUENCE 26 AA; 2880 MW; A5317FC47DDB8863 CRC64;

Query Match 85.0%; Score 17; DB 10; Length 26;
 Best Local Similarity 40.0%; Pred. No. 1.5e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 FXXXW 5
 Db 6 FTASW 10

RESULT 3
 ID 005602 PRELIMINARY; PRT; 32 AA.
 AC 005602:
 DT 01-JUL-1997 (TRENBLREL. 04, Created)
 DT 01-JUL-1997 (TRENBLREL. 04, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE Transposon Tn5041 DNA (Fragment).
 OS Pseudomonas sp.
 OC Bacteria; Proteobacteria.
 CX NCBI_TaxID=306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KHP41; TRANSPOSON-TN5041;
 RX MEDLINE=97419493; PubMed=9274008;
 RA Kholidil G.Y., Yurleva O.V., Gorlenko Z.M., Mindlin S.Z., Bass I.A.,
 RA Lomovskaya O.L., Kopleva A.V., Nikiforov V.G.;
 RT "Tn5041: a chimeric mercury resistance transposon closely related to
 the toluene degradative transposon Tn4651.";
 RL Microbiology 143:2549-2556(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KHP41; TRANSPOSON-TN5041;
 RA Kholidil G.Y., Mindlin S.Z., Gorlenko Z.M., Bass I.A., Kalyaeva E.S.,
 RA Nikiforov V.;
 RT "Host-dependent transposition of Tn5041.";
 RL Russ. J. Genet. 36:365-373(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KHP41; TRANSPOSON-TN5041;
 RA Kholidil G.Y.;
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X98999; CAA67458.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SO SEQUENCE 32 AA; 3298 MW; AFA2B5EP917077A CRC64;

Query Match 85.0%; Score 17; DB 2; Length 32;

Best Local Similarity 40.0%; Pred. No. 1.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 FXXXW 5
 Db 11 FSSSW 15

RESULT 4
 ID 09PV61 PRELIMINARY; PRT; 36 AA.
 AC 09PV61:
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE Dystrophin (Fragment).
 GN DYST.
 OS Mola mola (ocean sunfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Molidae; Mola.
 CX NCBI_TaxID=94237;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DYST6SUNFISH;
 RX MEDLINE=99398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate
 evolution.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL; AF137130; AAD54215.1; -.
 DR HSSP; P46939; IBHD.
 DR InterPro: IPR001715; Calponin-like.
 DR Pfam: PF00307; CH; 1.
 IT NON_TER 1
 IT NON_TER 1
 SO SEQUENCE 36 AA; 4181 MW; DE01642ABCAFC18 CRC64;

Query Match 85.0%; Score 17; DB 13; Length 36;
 Best Local Similarity 40.0%; Pred. No. 1.9e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 FXXXW 5
 Db 32 FSSSW 36

RESULT 5
 ID 09PV63 PRELIMINARY; PRT; 38 AA.
 AC 09PV63:
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE Dystrophin (Fragment).
 GN DYST.
 OS Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
 americanus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Pleuronectidae; Pleuronectidae; Pseudopleuronectes.
 CX NCBI_TaxID=8265;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DYST6FLOUNDER;
 RX MEDLINE=99398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate
 evolution.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL; AF137128; AAD54213.1; -.

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DR HSSP: P46939; IBHD.
DR InterPro: IPR001715; Calponin-like.
DR Pfam: PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 38
SQ SEQUENCE 38 AA: 4424 MW: 41C67E016A2A8CB0 CRC64:

Query Match
Best Local Similarity 85.0%; Score 17; DB 13; Length 38;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 32 FSSSW 36

RESULT 6
Q9PV89 PRELIMINARY; PRT; 40 AA.
AC Q9PV89:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN DYST.
OS Triakis sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes; Triakidae;
OC Triakis.
OC NCBI_TaxID=94228;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DYST6SHARK.
RA MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL: AF137083; AAD54177.1; -.
DR HSSP: P46939; IBHD.
DR InterPro: IPR001715; Calponin-like.
DR Pfam: PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA: 4604 MW: 796B35B9D1EB5569 CRC64:

Query Match
Best Local Similarity 85.0%; Score 17; DB 13; Length 40;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 32 FSSSW 36

RESULT 7
Q9PV88 PRELIMINARY; PRT; 40 AA.
AC Q9PV88:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN DYST.
OS Torpedo californica (Pacific electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hyposqualae; Pristiogaster; Batoidae;
OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
OC NCBI_TaxID=7787;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DYST6TORP.
RA MEDLINE=99398697; PubMed=10468597;

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RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL: AF137084; AAD54178.1; -.
DR HSSP: P46939; IBHD.
DR InterPro: IPR001715; Calponin-like.
DR Pfam: PF00307; CH; 1.
DR PROSITE: PS50021; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA: 4595 MW: 5E9B2565075B5576 CRC64:

Query Match
Best Local Similarity 85.0%; Score 17; DB 13; Length 40;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 32 FSSSW 36

RESULT 8
Q9PV85 PRELIMINARY; PRT; 40 AA.
AC Q9PV85:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN DYST.
OS Osteoglossum sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Osteoglossidae; Osteoglossum.
OC NCBI_TaxID=27725;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DYST6DRAGONFISH.
RA MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL: AF137087; AAD54181.1; -.
DR HSSP: P46939; IBHD.
DR InterPro: IPR001715; Calponin-like.
DR Pfam: PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA: 4598 MW: B48648166BDB57E5 CRC64:

Query Match
Best Local Similarity 85.0%; Score 17; DB 13; Length 40;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 32 FSSSW 36

RESULT 9
Q9PV84 PRELIMINARY; PRT; 40 AA.
AC Q9PV84:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN DYST.
OS Anguilla sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;

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CC Anguilla.
 CX NCBI_TaxID=62126;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DYST6EL;
 RX MEDLINE=9398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate evolution."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL; AF137088; AAD54182.1; -
 DR HSSP; P46939; 1BHD.
 DR InterPro; IPR001715; Calponin-like.
 DR Pfam; PF00307; CH; 1.
 DR PROSITE; PS50021; CH; 1.
 FT NON_TER 1
 FT NON_TER 40
 SQ SEQUENCE 40 AA; 4574 MW; 55784656BDB5437 CRC64;

Query Match 85.0%; Score 17; DB 13; Length 40;
 Best Local Similarity 40.0%; Pred. No. 2,1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 DB 32 FSSSW 36

RESULT 10

ID Q9PV82 PRELIMINARY; PRT; 40 AA.
 AC Q9PV82;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Dystrophin (Fragment).
 GN DYST.
 OS Barbus tetrazona.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Barbus.
 OX NCBI_TaxID=94221;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DYST6TIGERBAR;
 RX MEDLINE=9398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate evolution."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL; AF137090; AAD54184.1; -
 DR HSSP; P46939; 1BHD.
 DR InterPro; IPR001715; Calponin-like.
 DR Pfam; PF00307; CH; 1.
 FT NON_TER 1
 FT NON_TER 40
 SQ SEQUENCE 40 AA; 4573 MW; 459837C19BC3E736 CRC64;

Query Match 85.0%; Score 17; DB 13; Length 40;
 Best Local Similarity 40.0%; Pred. No. 2,1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 DB 32 FSSSW 36

RESULT 11

ID Q9PV81 PRELIMINARY; PRT; 40 AA.
 AC Q9PV81;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Dystrophin (Fragment).
 GN DYST.
 OS Esoc lucius (Northern pike).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Esociformes;
 OC Esocidae; Esoc.
 OX NCBI_TaxID=8010;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DYST6PIKE;
 RX MEDLINE=9398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate evolution."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL; AF137091; AAD54185.1; -
 DR HSSP; P46939; 1BHD.
 DR InterPro; IPR001715; Calponin-like.
 DR Pfam; PF00307; CH; 1.
 FT NON_TER 1
 FT NON_TER 40
 SQ SEQUENCE 40 AA; 4542 MW; 09165AA193794B14 CRC64;

Query Match 85.0%; Score 17; DB 13; Length 40;
 Best Local Similarity 40.0%; Pred. No. 2,1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 DB 32 FSSSW 36

RESULT 12

ID Q9PV80 PRELIMINARY; PRT; 40 AA.
 AC Q9PV80;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Dystrophin (Fragment).
 GN DYST.
 OS Plecoglossus altivelis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Proteocephalopterygii; Salmoniformes; Osmeridae; Plecoglossus.
 OX NCBI_TaxID=61084;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DYST6AYU;
 RX MEDLINE=9398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate evolution."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL; AF137092; AAD54186.1; -
 DR HSSP; P46939; 1BHD.
 DR InterPro; IPR001715; Calponin-like.
 DR Pfam; PF00307; CH; 1.
 FT NON_TER 1
 FT NON_TER 40
 SQ SEQUENCE 40 AA; 4512 MW; B4931BF59BDB542A CRC64;

Query Match 85.0%; Score 17; DB 13; Length 40;
 Best Local Similarity 40.0%; Pred. No. 2,1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 DB 32 FSSSW 36

RESULT 13

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Q9PT24
ID 09PT24 PRELIMINARY; PRT; 40 AA.
AC 09PT24;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN DYST.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DYST6PROUT;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137093; AAD54187.1; -.
DR HSSP; P46939; 1BHD.
DR InterPro: IPR001715; Calponin-like.
DR Pfam: PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4551 MW; B4865A19BDB4B17 CRC64;

Query Match
Best Local Similarity 85.0%; Score 17; DB 13; Length 40;
Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 32 FSSSW 36

RESULT 14
Q9PV79 PRELIMINARY; PRT; 40 AA.
AC 09PV79;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN DYST.
OS Galaxias maculatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Galaxiidae; Galaxias.
OX NCBI_TaxID=61620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DYST6GAL;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137094; AAD54188.1; -.
DR HSSP; P46939; 1BHD.
DR InterPro: IPR001715; Calponin-like.
DR Pfam: PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4613 MW; BA7C92D67E01642A CRC64;

Query Match
Best Local Similarity 85.0%; Score 17; DB 13; Length 40;
Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 32 FSSSW 36

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DB 32 FSSSW 36

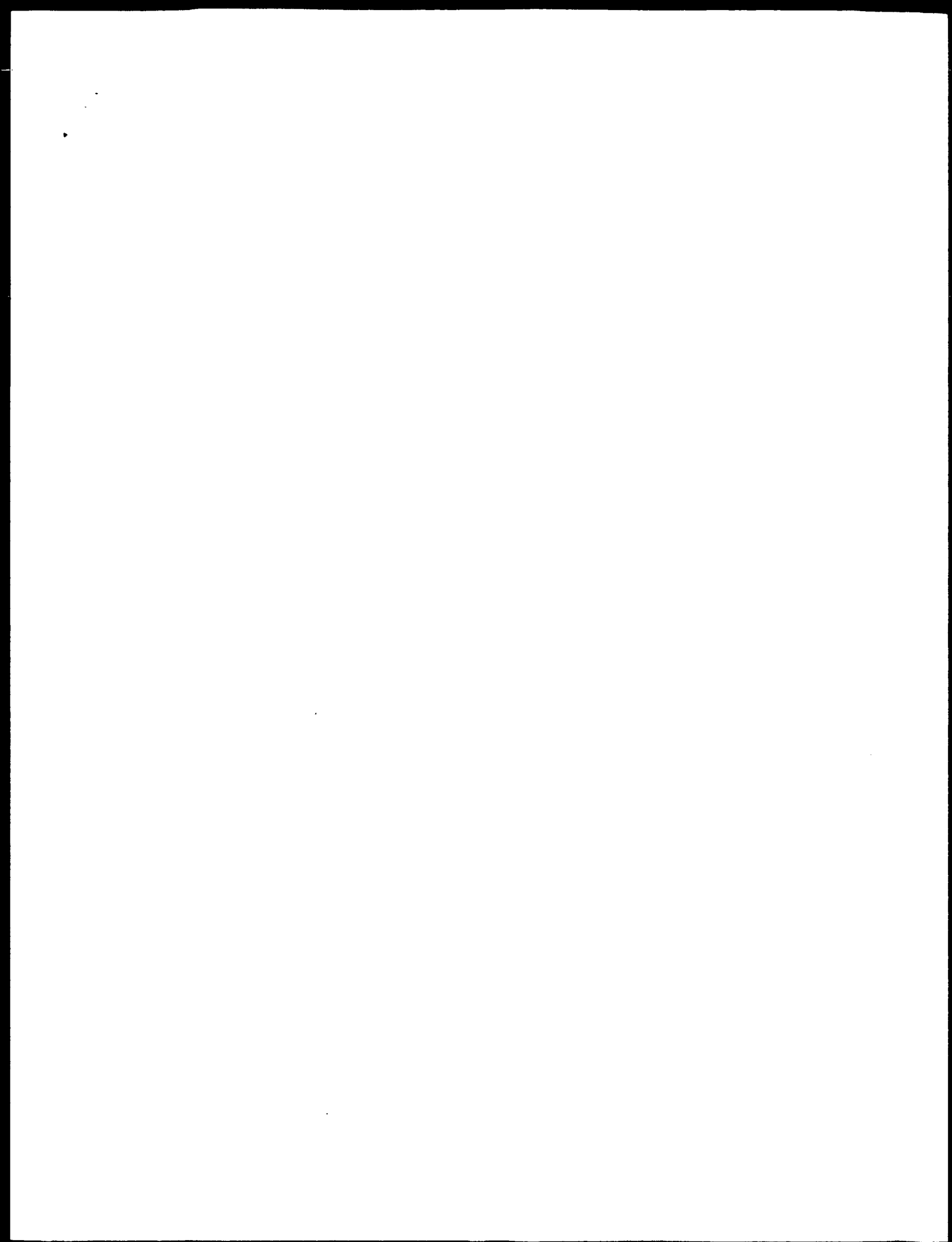
RESULT 15
Q9PU06 PRELIMINARY; PRT; 40 AA.
ID 09PU06;
AC 09PU06;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN DYST.
OS Lampiris sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Anthomorphia; Lampridiformes; Lamprididae; Lampiris.
OX NCBI_TaxID=94303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DYST6LAMP;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137096; AAD54189.1; -.
DR EMBL; AF137095; AAD54189.1; JOINED.
DR HSSP; P46939; 1BHD.
DR InterPro: IPR001715; Calponin-like.
DR Pfam: PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49DA9A67E01642A CRC64;

Query Match
Best Local Similarity 85.0%; Score 17; DB 13; Length 40;
Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 32 FSSSW 36

Search completed: January 29, 2003, 14:12:13
Job time : 30 secs

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PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
 PT pylori, comprises reacting a faecal sample with two binding reagents for
 PT antigens that survive intestinal passage -
 XX
 PS Claim 26; Page 22; 84pp; German.

CC This invention describes a novel method for the detection of a mammalian
 CC infection by an acid-resistant microorganism (A) by treating a faecal
 CC sample with at least two different monoclonal antibodies (MAb) (or their
 CC fragments or derivatives) or aptamers (collectively (I)) and detecting
 CC formation of a complex (C) between (I) and the corresponding antigen of
 CC (A). The first and second (I) bind to epitopes of different antigens
 CC (Ag). These epitopes are present, after passage through the intestines,
 CC in at least some mammals, and have either: (i) their native structure;
 CC or (ii) a structure against which an antibody is produced by an animal
 CC infected or immunized with (A), or its extract, lysate, derived protein
 CC or fragment, or with a synthetic peptide. Practically all mammals display
 CC at least one of the specified epitopes. The method is used to detect
 CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
 CC Mycobacterium and Campylobacter, particularly H. pylori, H. hepaticus,
 CC M. tuberculosis, C. jejuni and C. pylori. (I) may also be used
 CC therapeutically. The method is direct and non-invasive, and provides an
 CC inexpensive and easily standardizable diagnosis, despite possible
 CC degradation of antigens during passage through the intestines. This
 CC sequence represents a fragment of a H. pylori beta-urease-binding
 CC antibody heavy chain complementarity determining region CDRI which is
 CC used to illustrate the method of the invention.

CC Sequence 10 AA:

Query Match

Best Local Similarity 85.0%; Score 17; DB 21; Length 10;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXW 5
 DB 4 FSTW 8

RESULT 2

AAB86058
 ID AAB86058 standard; Peptide: 10 AA.

XX AAB86058;

XX 17-JUL-2001 (first entry)

XX H. pylori beta-urease derived antibody light chain CDRI #1.

XX Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;
 XX infection; acid-resistant microorganism; faecal; antibody; diagnosis;
 XX antibacterial; complementarity determining region.

XX Unidentified.

XX WO200127613-A2.

XX 19-APR-2001.

XX 12-OCT-2000; 2000WO-EP10058.

XX 12-OCT-1999; 99EP-0120351.

XX 16-MAR-2000; 2000EP-0105592.

XX 31-MAR-2000; 2000EP-0107028.

XX 10-MAY-2000; 2000EP-0101110.

XX (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

PI Reiter C, Cullmann G, Heppner P, Ringels A, Mueller H, Haindl E;
 DR WPI, 2001-282087/29.
 XX N-PSDB; AAF88060.

PT Detecting infections by acid-resistant microorganisms, particularly for
 PT diagnosis Helicobacter pylori, comprises an immunoassay on a faecal
 PT sample -
 XX
 PS Claim 23; Page 17; 89pp; German.

CC This invention describes a novel method for detecting, in a mammal,
 CC infection by an acid-resistant microorganism (A) which comprises reacting
 CC a faecal sample with: (i) a receptor (R) such that a complex is formed
 CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part
 CC complex is formed with Ag, and the formation of a complex detected. R are
 CC specific for an Ag which, after passage through the intestines, at least
 CC in some mammals, retains a native (or corresponding) structure against
 CC which the mammal produces antibodies (when immunized or infected with
 CC (A), or its extracts, lysates or derived proteins (or fragments) or
 CC synthetic peptides). The products of the invention have antibacterial
 CC activity. The method is used to diagnose infection by Helicobacter,
 CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
 CC H. hepaticus, C. jejuni and M. tuberculosis, and also to monitor the
 CC progress of treatment. Receptors, particularly antibodies, directed
 CC against Ag can be used therapeutically for treatment of infections. The
 CC method requires only one R to provide a reasonably secure diagnosis
 CC (although use of two R improves sensitivity), so is relatively
 CC inexpensive and more easily standardized. Also it is direct,
 CC non-invasive, suitable for automation and may indicate the stage of an
 CC infection. This sequence represents a complementarity determining region
 CC (CDR) from an antibody generated against a Helicobacter pylori antigen
 CC (catalase or beta-urease) which is used to illustrate the method of the
 CC invention.

CC Sequence 10 AA:

Query Match

Best Local Similarity 85.0%; Score 17; DB 22; Length 10;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXW 5
 DB 4 FSTW 8

RESULT 3

AAB86090
 ID AAB86090 standard; Peptide: 10 AA.

XX AAB86090;

XX 17-JUL-2001 (first entry)

XX H. pylori beta-urease derived antibody light chain CDRI #1.

XX Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
 XX acid-resistant microorganism; complementarity determining region;
 XX CDR; faeces; heavy chain; light chain.

XX Unidentified.

XX WO200127612-A2.

XX 19-APR-2001.

XX 12-OCT-2000; 2000WO-EP10057.

XX 12-OCT-1999; 99EP-0120351.

XX 16-MAR-2000; 2000EP-0105592.

XX 31-MAR-2000; 2000EP-0107028.

XX 10-MAY-2000; 2000EP-0101110.

XX (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

PI Reiter C, Cullmann G, Lakner M, Truue A, Dehnert S, Schwartz G;
 DR WPI, 2001-282086/29.

DR N-PSDB; AAF88117.
 XX Detecting infections by acid-resistant microorganisms, particularly for
 PT diagnosing *Helicobacter pylori*, comprises immunochromatographic
 PT detection of antigen in feces -
 PS Claim 27; Page 27; 90pp; German.
 XX
 XX This invention describes a novel method for detecting infection by an
 CC acid-resistant microorganism (A), in a mammal, using
 CC immunochromatography. The method is used to diagnose infection by an
 CC acid-resistant microorganism (A), in a mammal, such as *Helicobacter*,
 CC *Campylobacter* or *Mycobacterium*, particularly *H. pylori* (most preferred),
 CC *H. hepatica*, *C. jejuni* and *M. tuberculosis*. The method is rapid, simple,
 CC inexpensive and non-invasive, and may indicate the stage of infection.
 CC A test strip used in the method may include a filter to eliminate
 CC particles present in the sample and only a single receptor provides a
 CC reasonably secure diagnosis, with specificity and selectivity improved
 CC by detecting several epitopes (of catalase) or different antigens
 CC (catalase and beta-urease). The method can be automated. This sequence
 CC represents a complementarity determining region (CDR) from an antibody
 CC raised against the *H. pylori* catalase or beta-urease antigen which is
 CC used to illustrate the method of the invention.
 XX
 SO Sequence 10 AA:
 Query Match 85.0%; Score 17; DB 22; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.5e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 | |
 Db 4 FTSW 8
 RESULT 4
 AAE05735
 ID AAE05735 standard; peptide; 13 AA.
 XX
 AC AAE05735;
 XX
 DT 24-SEP-2001 (first entry)
 XX
 DE Complementarity-determining region 3 (CDR3) of MopHabs #7.
 XX
 DE Complementarity-determining region 3: monoclonal phage antibody;
 KW MopHabs; antigen.
 KW
 KM Synthetic.
 XX
 OS
 PN US6265150-B1.
 XX
 PD 24-JUL-2001.
 XX
 PF 26-MAY-1998; 98US-0085072.
 XX
 XX 07-JUN-1995; 95US-0483653.
 PR 18-SEP-1997; 97US-0932892.
 XX
 PA (BECT) BECTON DICKINSON & CO.
 PA (CRUC-) CRUCCELL HOLLAND BV.
 XX
 PI Terstappen LW, Logtenberg T;
 XX
 DR WPI; 2001-463929/50.
 XX
 PT Obtaining a phage particle, useful for obtaining human antibodies
 PT against known and novel surface antigens, by incubating a phage library
 PT with target cells to allow binding of the antibody fragment to the
 PT antigen -
 XX
 PS Example 6; Column 6; 6pp; English.
 XX

CC The invention relates to a method of obtaining a phage particle
 CC which has an antibody fragment directed against an antigen associated
 CC with the surface of target cells in a heterogeneous cell population.
 CC The method involves incubating a library of phage particles with the
 CC target cells to allow binding of the antibody fragment expressed on
 CC the surface of the phage particles to the antigen associated with
 CC the target cells. The method is useful for obtaining human antibodies
 CC against known and novel surface antigens in their native configuration,
 CC expressed on phenotypically defined subpopulations of cells.
 CC The present sequence is complementarity-determining region 3 (CDR3)
 CC of monoclonal phage antibodies (MopHabs) used in the exemplification
 CC of the invention.
 XX
 SO Sequence 13 AA:
 Query Match 85.0%; Score 17; DB 22; Length 13;
 Best Local Similarity 40.0%; Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 | |
 Db 6 FASSW 10
 RESULT 5
 AAM98088
 ID AAM98088 standard; peptide; 14 AA.
 XX
 AC AAM98088;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human peptide #1363 encoded by a SNP oligonucleotide.
 XX
 DE Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 KW
 OS Homo sapiens.
 XX
 PN W0200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-0535498.
 XX
 XX 28-DEC-1999; 99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI; 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 PS Disclosure; Page 3967; 4143pp; English.
 XX
 XX The present invention relates to oligonucleotides (see AUL26793-AUL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.

PD 22-MAY-1998.
 XX
 PF 12-NOV-1997; 97WO-JP04129.
 XX
 PR 13-NOV-1996; 96JP-0302053.
 XX
 PA (MEIP) MEIJI MILK PROD CO LTD.
 XX
 PI Dairiki K, Kino K, Kume A, Sone T;
 XX
 PS WPI; 1998-297617/26.
 DR
 XX Peptides derived from Japanese cedar pollen antigens are
 PT immunotherapeutic agents - useful for allergy treatment and typing
 PT HLA Class II molecules in allergy sufferers
 XX
 PS Claim 12; Page 29; 50pp; Japanese.
 CC This sequence represents residues 16-30 of the Cry j 2 protein, and
 CC is a peptide of the invention. The peptides are derived from Japanese
 CC cedar pollen antigens, and are used as immunotherapeutic agents in the
 CC treatment of allergy. The peptides can be used for identification and
 CC typing of the particular HLA class II molecules in an allergy sufferer,
 CC and also for peptide immunotherapy of an allergy. Using these peptides
 CC the immunotherapy can be targeted more specifically to the requirements
 CC of the individual patient, allowing more effective treatment of an
 CC allergy, including those patients for whom treatment with a conventional
 CC immunotherapeutic agent is ineffective.
 XX
 SO Sequence 15 AA;
 Query Match 85.0%; Score 17; DB 19; Length 15;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FXXXW 5
 | |
 Db 9 FSTAW 13
 RESULT 9
 AAE23038
 ID AAE23038 standard; peptide; 19 AA.
 XX
 AC AAE23038;
 XX
 DT 21-AUG-2002 (first entry)
 XX
 DE Human thiorodoxin, 47916 peptide.
 XX
 KW Human: thiorodoxin; 22108; 47916; haematopoietic disorder; leukaemia;
 KW cancer; lung; breast; thyroid; head; neck; prostate; genitourinary tract;
 KW cardiovascular disease; angina pectoris; arteriosclerosis; heart failure;
 KW brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma;
 KW cystostatic; carcinoma; cardiac; neuroprotective; antiinflammatory;
 KW gene therapy; nootropic.
 XX
 KM Homo sapiens.
 XX
 OS WO200226803-A2.
 PN
 XX
 PD 04-APR-2002.
 XX
 PF 25-SEP-2001; 2001WO-US29967.
 XX
 PR 25-SEP-2000; 2000US-235049P.
 XX
 PA (MILL-) MILLENITUM PHARM INC.
 XX
 PI Bandaru R, Kapeller-Libermann R;
 XX
 DR WPI; 2002-416475/44.
 XX

PT New human thiorodoxin nucleic acid and polypeptide molecules,
 PT designated 22108 and 47916, useful for diagnosing, preventing or
 PT treating cancer (e.g. carcinoma), cardiovascular diseases (e.g. heart
 PT failure) or brain disorders
 XX
 PS Disclosure; Page 11; 124pp; English.
 XX
 CC The invention relates to human thiorodoxin nucleic acid and polypeptide
 CC molecules, designated 22108 and 47916. The compound that modulates the
 CC activity or expression of 22108 and 47916 nucleic acid is useful for
 CC treating or preventing a disorder characterised by aberrant activity of
 CC 22108 and 47916-expressing cell, specifically for reducing or inhibiting
 CC the aberrant activity of the 22108 and 47916-expressing cancer cell. The
 CC 22108 and 47916 nucleic acid and polypeptide are useful for diagnosing,
 CC preventing or treating cancer in a subject (e.g. carcinoma, sarcoma,
 CC metastatic or haematopoietic disorders (e.g. leukaemia), or cancers of
 CC the lung, breast, thyroid, head neck, prostate or genito-urinary tract),
 CC cardiovascular diseases (e.g. angina pectoris, arteriosclerosis or heart
 CC failure) or brain disorders (e.g. brain abscess, meningitis, Alzheimer's
 CC diseases). The thiorodoxin DNA is also useful in gene therapy. The
 CC present sequence is human thiorodoxin, 47916 peptide.
 XX
 SO Sequence 19 AA;
 Query Match 85.0%; Score 17; DB 23; Length 19;
 Best Local Similarity 40.0%; Pred. No. 2.5e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FXXXW 5
 | |
 Db 4 FSATW 8
 RESULT 10
 AAM42165
 ID AAM42165 standard; peptide; 20 AA.
 XX
 AC AAM42165;
 XX
 DT 16-JUN-1998 (first entry)
 XX
 DE T-cell epitope peptide 45 from Japanese cypress pollen antigen Chao2.
 XX
 KW Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2;
 KW diagnosis; allergy; spring tree pollen disease; pollinosis.
 XX
 OS Chamaecyparis obtusa.
 XX
 OS WO9747648-A1.
 PN
 XX
 PD 18-DEC-1997.
 XX
 PF 12-JUN-1997; 97WO-JP02031.
 XX
 PR 14-JUN-1996; 96JP-0153527.
 XX
 PA (MEIP) MEIJI MILK PROD CO LTD.
 XX
 PI Dairiki K, Kino K;
 XX
 PS WPI; 1998-052242/05.
 DR
 XX
 PD T-cell epitope peptide portion of Japanese cypress pollen antigens
 PT Chao1 and Chao2 - used for diagnosis and treatment of spring tree
 PT pollen disease
 XX
 PS Claim 2; Page 36; 71pp; Japanese.
 XX
 CC The present sequence represents a T-cell epitope peptide from Japanese
 CC cypress pollen antigen Chao2. The present invention describes peptides
 CC which correspond to the T-cell epitope sites on Japanese cypress pollen
 CC antigens Chao1 and Chao2. The peptides can be used as a reagent for the
 CC diagnosis of allergy to Japanese cypress pollen, and as an antigen in

XX AAM31077;
 AC 17-OCT-2001 (first entry)
 DT
 XX Peptide #5114 encoded by probe for measuring placental gene expression.
 DE
 XX Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 XX
 OS Homo sapiens.
 XX WO200157272-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US00663.
 PF
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488897/53.
 DR
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human placenta -
 CC
 XX Claim 27; SEQ ID No 31346; 654bp; English.
 PS
 CC The present invention relates to single exon nucleic acid probes (SENP;
 CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.
 CC
 SQ Sequence 27 AA:
 Query Match 85.0%; Score 17; DB 23; Length 27;
 Best Local Similarity 40.0%; Pred. No. 3.3e+03;
 Matches 2: Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FXXW 5
 1 1
 4 FSATW 8
 DB
 RESULT 14
 ABG40522
 ID ABG40522 standard; Peptide: 27 AA.
 XX
 AC ABG40522;
 XX
 DT 19-AUG-2002 (first entry)
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 30187.
 XX
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;

KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX WO200186003-A2.
 PN
 XX 15-NOV-2001.
 PD
 XX 30-JAN-2001; 2001WO-US00665.
 PF
 XX 04-FEB-2000; 2000US-180312P.
 PR 26-MAY-2000; 2000US-207456P.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 DR
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples -
 CC
 XX Claim 27; SEQ ID No 30187; 634bp; English.
 PS
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 1614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 1614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes. The novel set of probes which hybridize at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a peptide/protein
 CC encoded by a single exon probe of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 SQ Sequence 27 AA:
 Query Match 85.0%; Score 17; DB 23; Length 27;

Best Local Similarity 40.0%; Pred. No. 3.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FXXXW 5
 4 FSATW 8
 Db

Search completed: January 29, 2003, 14:11:20
 Job time : 36 secs

RESULT 15
 AAB09301 standard; Protein; 29 AA.
 ID AAB09301
 XX
 AC AAB09301;
 XX
 DT 30-AUG-2000 (first entry)
 XX
 DE Hepatitis GB virus protein sequence SEQ ID NO:428.
 XX
 KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic;
 XX infection; detection; characterisation; hepatitis.
 OS Hepatitis GB virus.
 XX
 PN US6051374-A.
 XX
 PD 18-APR-2000.
 XX
 PE 07-JUN-1995; 95US-0488445.
 XX
 PR 14-FEB-1994; 94US-0196030.
 PR 13-MAY-1994; 94US-0242654.
 PR 29-JUL-1994; 94US-0283314.
 PR 23-NOV-1994; 94US-0344185.
 PR 23-NOV-1994; 94US-0344190.
 PR 30-JAN-1995; 95US-0377557.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
 PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder CG;
 XX
 DR WPI; 2000-338307/29.
 XX
 XX Detecting target hepatitis GB virus nucleic acid in a test sample
 PT suspected of containing HGBV comprises reacting the test sample the
 PT HGBV polynucleotide probe and detecting the complex that contains
 PT target HGBV -
 XX
 PS Example 18; Column 491-492; 369pp; English.
 XX
 CC The present invention describe a method for detecting target
 CC hepatitis GB virus (HGBV) nucleic acid (THN) in a test sample (T)
 CC suspected of containing HGBV. The method involves reacting (T) with a
 CC HGBV polynucleotide probe (I) containing 15 contiguous nucleotides, and
 CC which selectively hybridises to the HGBV genome or its full complement,
 CC and detecting the complex that contains THN, indicating the presence of
 CC target HGBV. The method is used for detecting target HGBV nucleic acid
 CC in the test sample suspected of containing HGBV and for characterisation
 CC of newly ascertained etiological agent of non-A, non-B, non-C, non-D and
 CC non-E hepatitis causing agents collectively termed as hepatitis GB
 CC virus. AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide
 CC and protein sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 29 AA;

Query Match 85.0%; Score 17; DB 21; Length 29;
 Best Local Similarity 40.0%; Pred. No. 3.5e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 12 FASAW 16
 Db

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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:12:18 ; Search time 11 Seconds
(without alignments)
9.172 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published_Applications_AA.*
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3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
11: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	85.0	27	10	US-09-864-761-46828
2	17	85.0	29	8	US-08-424-5508-428
3	17	85.0	40	10	US-09-057-951-6
4	17	85.0	40	10	US-09-864-761-46093
5	17	85.0	40	12	US-10-105-150-6
6	17	85.0	44	10	US-09-864-761-35268
7	17	85.0	46	10	US-09-864-761-35084
8	17	85.0	71	10	US-09-864-761-45867
9	17	85.0	75	10	US-09-867-550-510
10	17	85.0	77	12	US-10-001-843-186
11	17	85.0	78	10	US-09-864-761-33877
12	17	85.0	104	9	US-10-032-482-1
13	17	85.0	111	10	US-09-825-300-980
14	17	85.0	114	10	US-09-897-898-6
15	17	85.0	114	10	US-09-992-524-9
16	17	85.0	114	10	US-09-992-524-10
17	17	85.0	114	10	US-09-992-524-11
18	17	85.0	125	10	US-09-925-300-1114
19	17	85.0	134	9	US-10-079-623-364

20	17	85.0	135	10	US-09-925-299-878	Sequence 878, App
21	17	85.0	136	10	US-09-992-524-4	Sequence 4, Appli
22	17	85.0	136	10	US-09-992-524-8	Sequence 8, Appli
23	17	85.0	169	10	US-09-897-898-9	Sequence 9, Appli
24	17	85.0	174	10	US-09-764-877-1745	Sequence 1745, Ap
25	17	85.0	181	8	US-08-870-434-10	Sequence 10, Appl
26	17	85.0	182	8	US-08-825-486-8	Sequence 8, Appli
27	17	85.0	182	10	US-09-372-044-8	Sequence 3, Appli
28	17	85.0	192	10	US-09-864-761-33690	Sequence 33690, A
29	17	85.0	232	10	US-09-897-898-11	Sequence 11, Appli
30	17	85.0	241	10	US-09-815-242-10985	Sequence 10985, A
31	17	85.0	247	9	US-09-908-193-42	Sequence 42, Appli
32	17	85.0	248	9	US-09-908-193-16	Sequence 16, Appli
33	17	85.0	249	9	US-09-908-193-16	Sequence 6, Appli
34	17	85.0	258	9	US-09-813-453A-6	Sequence 1258, Ap
35	17	85.0	268	10	US-09-764-864-1258	Sequence 1433, Ap
36	17	85.0	270	10	US-09-764-864-1433	Sequence 294, Appl
37	17	85.0	271	9	US-09-479-040-23	Sequence 23, Appli
38	17	85.0	273	10	US-09-893-737-294	Sequence 294, Appl
39	17	85.0	289	10	US-09-815-242-5556	Sequence 5556, Ap
40	17	85.0	293	10	US-09-925-301-1119	Sequence 1119, Ap
41	17	85.0	297	9	US-09-738-626-6265	Sequence 6265, Ap
42	17	85.0	313	10	US-09-886-055-415	Sequence 415, App
43	17	85.0	324	10	US-09-966-264-31	Sequence 31, Appl
44	17	85.0	328	10	US-09-815-242-12495	Sequence 12495, A
45	17	85.0	345	9	US-10-007-706-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-864-761-46828
Sequence 46828, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmics-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 46828
LENGTH: 27
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007739.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.62
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.66
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.68
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.61
US-09-864-761-46828

Query Match 85.0%; Score 17; DB 10; Length 27;
Best Local Similarity 40.0%; Pred. No. 5.7e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 FXXXW 5
Dt 4 FSAW 8

RESULT 2
US-08-424-550B-428
Sequence 428, Application US/08424550B
Patent No. US20020119447A1
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BULLER
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: POROMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 428:

SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-428

Query Match 85.0%; Score 17; DB 8; Length 29;
Best Local Similarity 40.0%; Pred. No. 6e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 FXXXW 5
Db 12 FASAW 16

RESULT 3
US-09-057-951-6
Sequence 6, Application US/09057951
Patent No. US20020025551A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,951
FILING DATE: 09-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Melkijohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-057-951-6

Query Match 85.0%; Score 17; DB 10; Length 40;
Best Local Similarity 40.0%; Pred. No. 7.4e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 FXXXW 5
Db 6 FSAW 10

RESULT 4
US-09-864-761-46093
Sequence 46093, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.

```

APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 46093
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AF233390.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
US-09-864-761-46093

Query Match      85.0%: Score 17; DB 10; Length 40;
Best Local Similarity 40.0%: Pred. No. 7.4e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/105,150
FILING DATE: 25-Mar-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/057,951
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-105-150-6

Query Match      85.0%: Score 17; DB 12; Length 40;
Best Local Similarity 40.0%: Pred. No. 7.4e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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US-09-864-761-35268
Sequence 35268, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30

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US-10-105-150-6
Sequence 35268, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30

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/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 35268
/ LENGTH: 44
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC004852.2
/ OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
/ OTHER INFORMATION: EST_HUMAN HIT: AA320774.1, EVALUATE 5.00e-10
/ OTHER INFORMATION: SWISSPROT HIT: P11369, EVALUATE 1.00e-03
US-09-864-761-35268

Query Match      85.0%  Score 17;  DB 10;  Length 44;
Best Local Similarity 40.0%;  Pred. No. 7.9e+02;
Matches 2: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 18 PAATW 22

RESULT 7
US-09-864-761-35084
/ Sequence 35084, Application US/09864761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ FILE REFERENCE: Acomica-x-1
/ CURRENT FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US/09/864,761
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263,6
/ PRIOR FILING DATE: 2000-10-04
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/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 35084
/ LENGTH: 46
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC007938.1
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
/ OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.7
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
/ OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.6
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.99
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
/ OTHER INFORMATION: EST_HUMAN HIT: BF642802.1, EVALUATE 2.00e-19
/ OTHER INFORMATION: SWISSPROT HIT: P53620, EVALUATE 5.00e-15
US-09-864-761-35084

Query Match      85.0%  Score 17;  DB 10;  Length 46;
Best Local Similarity 40.0%;  Pred. No. 8.1e+02;
Matches 2: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 20 FAAMW 24

RESULT 8
US-09-864-761-45867
/ Sequence 45867, Application US/09864761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
/ FILE REFERENCE: Acomica-x-1
/ CURRENT FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US/09/864,761
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-05-26
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  PRIOR APPLICATION NUMBER: US 09/632,366
  PRIOR FILING DATE: 2000-08-03
  PRIOR APPLICATION NUMBER: GB 24263.6
  PRIOR FILING DATE: 2000-10-04
  PRIOR APPLICATION NUMBER: US 60/236,359
  PRIOR FILING DATE: 2000-09-27
  PRIOR APPLICATION NUMBER: PCT/US01/00666
  PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00667
  PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00664
  PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00669
  PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00665
  PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00668
  PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00663
  PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00662
  PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00661
  PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00670
  PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: US 60/234,687
  PRIOR FILING DATE: 2000-09-21
  PRIOR APPLICATION NUMBER: US 09/608,408
  PRIOR FILING DATE: 2000-06-30
  PRIOR APPLICATION NUMBER: US 09/774,203
  PRIOR FILING DATE: 2001-01-29
  NUMBER OF SEQ ID NOS: 49117
  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
  SEQ ID NO 45867
  LENGTH: 71
  TYPE: PRT
  ORGANISM: Homo sapiens
  FEATURE:
  OTHER INFORMATION: MAP TO AL121827.9
  OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.61
  OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
  OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.58
  OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.51
  OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.51
  OTHER INFORMATION: SWISSPROT HIT: Q63262, EVALUATE 4.40e-01
  OTHER INFORMATION: EST_HUMAN HIT: AW151498.1, EVALUATE 1.00e+00
  US-09-864-761-45867

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Query Match      85.0%  Score 17;  DB 10;  Length 71;
Best Local Similarity 40.0%  Pred. No. 1.1e+03;
Matches 2;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

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QY 1 FXXXW 5
Db 4 FASW 8

RESULT 9
US-09-867-550-510
; Sequence 510, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehriban, Fnuad
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20

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; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 510
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-867-550-510

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Query Match      85.0%  Score 17;  DB 10;  Length 75;
Best Local Similarity 40.0%  Pred. No. 1.1e+03;
Matches 2;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

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QY 1 FXXXW 5
Db 64 FSSW 68

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RESULT 10
US-10-001-843-186
; Sequence 186, Application US/10001843
; Patent No. US20020132255A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herive
; APPLICANT: Caferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chonghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and
; FILE REFERENCE: DEX-0267
; CURRENT APPLICATION NUMBER: US/10/001,843
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/249,992
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 186
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-001-843-186

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Query Match      85.0%  Score 17;  DB 12;  Length 77;
Best Local Similarity 40.0%  Pred. No. 1.1e+03;
Matches 2;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

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QY 1 FXXXW 5
Db 63 FASW 67

RESULT 11
US-09-864-761-33877
; Sequence 33877, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366

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; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33877
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007600.2
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.81
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.97
; OTHER INFORMATION: EST_HUMAN HIT: BE089591.1, EVALUATE 4.00e-09
; OTHER INFORMATION: SWISSPROT HIT: O15440, EVALUATE 2.00e-08
US-09-864-761-33877

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Query Match      85.0%; Score 17; DB 10; Length 78;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXW 5
Db 39 FSSW 43

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RESULT 12
US-10-032-482-1
; Sequence 1, Application US/10032482
; Publication No. US20020197270A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irum
; APPLICANT: KOTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUIZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR

```

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; TITLE OF INVENTION: IMMUNITY
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/10/032,482
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US/09/445,602
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-032-482-1

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Query Match      85.0%; Score 17; DB 9; Length 104;
Best Local Similarity 40.0%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXW 5
Db 20 FTSSW 24

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```

RESULT 13
US-09-925-300-980
; Sequence 980, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 980
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-980

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Query Match      85.0%; Score 17; DB 10; Length 111;
Best Local Similarity 40.0%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXW 5
Db 52 FAASW 56

```

```

RESULT 14
US-09-897-898-6
; Sequence 6, Application US/09897898
; Patent No. US20020037303A1
; GENERAL INFORMATION:
; APPLICANT: DECKERS, HARM M.
; APPLICANT: VAN ROOIJEN, GIJS
; APPLICANT: BOOTHIE, JOSEPH
; APPLICANT: GOLD, JANIS
; APPLICANT: MOLONEY, MAURICE M.

```

APPLICANT: DALMIA, BIPIN K.
 TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
 FILE REFERENCE: 034547/0104
 CURRENT APPLICATION NUMBER: US/09/897,898
 PRIOR FILING DATE: 2001-09-21,147
 PRIOR APPLICATION NUMBER: 09/577,147
 PRIOR FILING DATE: 2000-05-24
 PRIOR APPLICATION NUMBER: 09/448,600
 PRIOR FILING DATE: 1999-11-24
 PRIOR APPLICATION NUMBER: 09/084,777
 PRIOR FILING DATE: 1998-05-27
 PRIOR APPLICATION NUMBER: 60/047,753
 PRIOR FILING DATE: 1997-05-27
 PRIOR APPLICATION NUMBER: 60/047,779
 PRIOR FILING DATE: 1997-05-28
 PRIOR APPLICATION NUMBER: 60/075,863
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/075,864
 PRIOR FILING DATE: 1998-02-25
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 6
 LENGTH: 114
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 US-09-897-898-6

Query Match 85.0%; Score 17; DB 10; Length 114;
 Best Local Similarity 40.0%; Pred. No. 1.5e+03;
 Matches 2: Conservative 0; Mismatches 3; Indels 0; Caps 0;

OY 1 FXXW 5
 Db 35 FTASW 39

RESULT 15
 US-09-992-524-9
 Sequence 9, Application US/09992524
 Patent No. US20020091240A1
 GENERAL INFORMATION:
 APPLICANT: Vasquez, Maximiliano
 APPLICANT: Landolfi, Nicholas F.
 APPLICANT: Tsurushita, Naoya
 APPLICANT: Queen, Cary L.
 APPLICANT: Protein Design Labs, Inc.
 TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
 FILE REFERENCE: 011823-008110US
 CURRENT APPLICATION NUMBER: US/09/992,524
 CURRENT FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: 09/450,520
 PRIOR FILING DATE: 1999-11-29
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 9
 LENGTH: 114
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:humanized
 OTHER INFORMATION: Immunoglobulin huxAF
 US-09-992-524-9

Query Match 85.0%; Score 17; DB 10; Length 114;
 Best Local Similarity 40.0%; Pred. No. 1.5e+03;
 Matches 2: Conservative 0; Mismatches 3; Indels 0; Caps 0;

OY 1 FXXW 5
 Db 29 FTSSW 33

100

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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:11:27 ; Search time 138 Seconds
(without alignments)
23.360 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20

Sequence: 1 FXXXW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents-AA-Main:*

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19: /cgn2_6/ptodata/1/paa/US103.COMB.pep.*
20: /cgn2_6/ptodata/1/paa/US104.COMB.pep.*
21: /cgn2_6/ptodata/1/paa/US105.COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US106.COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US107.COMB.pep.*
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25: /cgn2_6/ptodata/1/paa/US109.COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US110.COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US111.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	85.0	9	24	US-10-072-419-3
2	17	85.0	9	24	US-10-072-419-8
3	17	85.0	10	22	US-09-842-776A-28
4	17	85.0	10	24	US-10-089-452-36
5	17	85.0	10	25	US-10-110-410-36
6	17	85.0	11	24	US-10-072-419-37

7	17	85.0	14	17	US-09-355-397C-36	Sequence 36, Appl
8	17	85.0	15	17	US-09-308-027-12	Sequence 12, Appl
9	17	85.0	15	17	US-09-308-027-88	Sequence 88, Appl
10	17	85.0	15	17	US-09-308-027A-12	Sequence 12, Appl
11	17	85.0	15	17	US-09-308-027A-88	Sequence 88, Appl
12	17	85.0	15	17	US-09-308-027A-88	Sequence 10, Appl
13	17	85.0	19	23	US-09-963-339-10	Sequence 59, Appl
14	17	85.0	19	25	US-10-145-586-59	Sequence 45, Appl
15	17	85.0	20	16	US-09-240-203B-265	Sequence 265, Appl
16	17	85.0	20	16	US-09-240-203D-265	Sequence 265, Appl
17	17	85.0	20	16	US-09-240-203D-265	Sequence 95, Appl
18	17	85.0	21	4	US-08-074-1808-95	Sequence 275, Appl
19	17	85.0	22	7	US-08-344-185C-275	Sequence 264, Appl
20	17	85.0	24	16	US-09-240-203B-264	Sequence 264, Appl
21	17	85.0	24	16	US-09-240-203D-264	Sequence 264, Appl
22	17	85.0	27	1	PCT-US01-000663-31346	Sequence 31346, A
23	17	85.0	27	22	US-09-864-761-46828	Sequence 46828, A
24	17	85.0	27	25	US-10-182-997-23443	Sequence 23443, A
25	17	85.0	27	26	US-10-203-135-30187	Sequence 30187, A
26	17	85.0	27	26	US-10-203-136-31135	Sequence 31135, A
27	17	85.0	27	26	US-10-203-137-31346	Sequence 31346, A
28	17	85.0	27	27	US-09-240-203D-265	Sequence 21109, A
29	17	85.0	28	27	US-09-240-203D-265	Sequence 3999, A
30	17	85.0	29	8	US-08-424-550A-428	Sequence 428, A
31	17	85.0	29	8	US-08-424-550B-428	Sequence 428, A
32	17	85.0	29	8	US-08-467-344A-428	Sequence 428, A
33	17	85.0	29	8	US-08-467-344A-428	Sequence 428, A
34	17	85.0	29	8	US-08-467-344A-428	Sequence 428, A
35	17	85.0	29	8	US-08-467-344A-428	Sequence 428, A
36	17	85.0	30	21	US-09-758-462-1651	Sequence 1651, A
37	17	85.0	30	26	US-10-212-059-1651	Sequence 1651, A
38	17	85.0	32	1	PCT-US00-29360-216	Sequence 28347, A
39	17	85.0	33	24	US-10-029-386-28347	Sequence 28347, A
40	17	85.0	33	24	US-10-032-201B-157	Sequence 157, A
41	17	85.0	34	20	US-09-614-450-3288	Sequence 3288, A
42	17	85.0	35	20	US-09-614-450-3288	Sequence 10658, A
43	17	85.0	36	3	PCT-US93-11000-5	Sequence 5, Appl
44	17	85.0	36	3	US-07-975-179A-5	Sequence 5, Appl
45	17	85.0	36	6	US-08-226-248A-137	Sequence 137, Appl

ALIGNMENTS

RESULT 1
US-10-072-419-3
Sequence 3, Application US/10072419
GENERAL INFORMATION:
APPLICANT: Schacter, Lee
TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in H
FILE REFERENCE: 10739-1
CURRENT APPLICATION NUMBER: US/10/072,419
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 9
TYPE: PRT
ORGANISM: Apis mellifera
US-10-072-419-3

Query Match 85.0%; Score 17; DB 24; Length 9;
Best Local Similarity 40.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 4 FTSSW 8

RESULT 2
US-10-072-419-8

```
; Sequence 8, Application US/10072419
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Huma
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072.419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-072-419-8
```

```
Query Match
Best Local Similarity 85.0%; Score 17; DB 24; Length 9;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
CY 1 FXXXW 5
| |
DB 4 FTSW 8
```

```
RESULT 3
US-09-842-776A-28
; Sequence 28, Application US/09842776A
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842.776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarily determining region (CDR1) of an
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease
US-09-842-776A-28
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Query Match
Best Local Similarity 85.0%; Score 17; DB 22; Length 10;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
OY 1 FXXXW 5
| |
DB 4 FTSW 8
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RESULT 4
US-10-089-452-36
; Sequence 36, Application US/10089452
; GENERAL INFORMATION:
; APPLICANT: Connex Gesellschaft zur Optimierung von Forschung und Entwicklung mbH
; TITLE OF INVENTION: Improved Method for Detecting Acid Resistant Microorganisms in th
; FILE REFERENCE: D 2394 PCT
; CURRENT APPLICATION NUMBER: US/10/089.452
; CURRENT FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR
US-10-089-452-36
```

```
Query Match
Best Local Similarity 85.0%; Score 17; DB 24; Length 10;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 FXXXW 5
| |
DB 4 FTSW 8
```

```
RESULT 5
US-10-110-410-36
; Sequence 36, Application US/10110410
; GENERAL INFORMATION:
; APPLICANT: Connex Gesellschaft zur Optimierung von Forschung und Entwicklung mbH
; TITLE OF INVENTION: Immunochromatographic Rapid Test for Detecting Acid Resistant
; FILE REFERENCE: D 1805 PCT
; CURRENT APPLICATION NUMBER: US/10/110.410
; CURRENT FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR
US-10-110-410-36
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```
Query Match
Best Local Similarity 85.0%; Score 17; DB 25; Length 10;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
OY 1 FXXXW 5
| |
DB 4 FTSW 8
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```
RESULT 6
US-10-072-419-37
; Sequence 37, Application US/10072419
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in H
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072.419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-072-419-37
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```
Query Match
Best Local Similarity 85.0%; Score 17; DB 24; Length 11;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
OY 1 FXXXW 5
| |
DB 4 FTSW 8
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```
RESULT 7
US-09-355-397C-36
; Sequence 36, Application US/09355397C
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```

; GENERAL INFORMATION:
; APPLICANT: Spyrou, Giannis
; TITLE OF INVENTION: Mammalian Thiredoxin
; FILE REFERENCE: 102043-100
; CURRENT APPLICATION NUMBER: US/09/355.397C
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/GB98/00263
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: GB 9701710.7
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 36
; LENGTH: 14
; TYPE: PRT
; ORGANISM: mammal
; US-09-355-397C-36
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Query Match      85.0%; Score 17; DB 17; Length 14;
Best Local Similarity 40.0%; Pred. No. 2e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 FXXXW 5
        |  |
Db       5 FSAW 9
```

```

RESULT 8
US-09-308-027-12
; Sequence 12, Application US/09308027
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Daijiki, Kazuo
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
; FILE REFERENCE: 06501/031001
; CURRENT APPLICATION NUMBER: US/09/308.027
; CURRENT FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: PCT/JP97/04129
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: JP 8/302053
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria
; US-09-308-027-12
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Query Match      85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 FXXXW 5
        |  |
Db       9 FSTAW 13
```

```

RESULT 9
US-09-308-027-88
; Sequence 88, Application US/09308027
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Daijiki, Kazuo
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
; FILE REFERENCE: 06501/031001
; CURRENT APPLICATION NUMBER: US/09/308.027
; CURRENT FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: PCT/JP97/04129
```

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; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: JP 8/302053
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 88
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria
; US-09-308-027-88
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Query Match      85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 FXXXW 5
        |  |
Db       4 FSTAW 8
```

```

RESULT 10
US-09-308-027A-12
; Sequence 12, Application US/09308027A
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Daijiki, Kazuo
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
; FILE REFERENCE: 06501/031001
; CURRENT APPLICATION NUMBER: US/09/308.027A
; CURRENT FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: PCT/JP97/04129
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: JP 8/302053
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria
; US-09-308-027A-12
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Query Match      85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 FXXXW 5
        |  |
Db       9 FSTAW 13
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```

RESULT 11
US-09-308-027A-88
; Sequence 88, Application US/09308027A
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Daijiki, Kazuo
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
; FILE REFERENCE: 06501/031001
; CURRENT APPLICATION NUMBER: US/09/308.027A
; CURRENT FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: PCT/JP97/04129
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: JP 8/302053
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 88
; LENGTH: 15
```

TYPE: PRT
ORGANISM: Cryptomeria
US-09-308-027A-88

Query Match 85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 4 FSATW 8

RESULT 12
US-09-963-339-10
Sequence 10, Application US/09963339
GENERAL INFORMATION:
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN
FILE REFERENCE: 10448-090001
CURRENT APPLICATION NUMBER: US/09/963,339
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/235,049
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-09-963-339-10

Query Match 85.0%; Score 17; DB 23; Length 19;
Best Local Similarity 40.0%; Pred. No. 2.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 4 FSATW 8

RESULT 13
US-10-145-586-59
Sequence 59, Application US/10145586
GENERAL INFORMATION:
APPLICANT: Alexandra Glucksmann, Maria
APPLICANT: Silos-Santiago, Immaculada
APPLICANT: M. Galvin, Katherine
APPLICANT: Welch, Nadine
APPLICANT: Curtis, Rory A.J.
APPLICANT: Bandaru, Rajasekhar
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
FILE REFERENCE: 10448-188001
CURRENT APPLICATION NUMBER: US/10/145,586
CURRENT FILING DATE: 2002-05-14
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 95
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 59
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-10-145-586-59

Query Match 85.0%; Score 17; DB 25; Length 19;
Best Local Similarity 40.0%; Pred. No. 2.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

DB 4 FSATW 8

RESULT 14
US-09-202-464-45
Sequence 45, Application US/09202464
GENERAL INFORMATION:
APPLICANT: Kino, Kousuke
APPLICANT: Dairiki, Kazuo
TITLE OF INVENTION: T-CELL EPITOPE PEPTIDES
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/202,464
FILING DATE: 14-Dec-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO JP97/02031
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: JP 8/153527
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06501-024001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-202-464-45

Query Match 85.0%; Score 17; DB 16; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.5e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

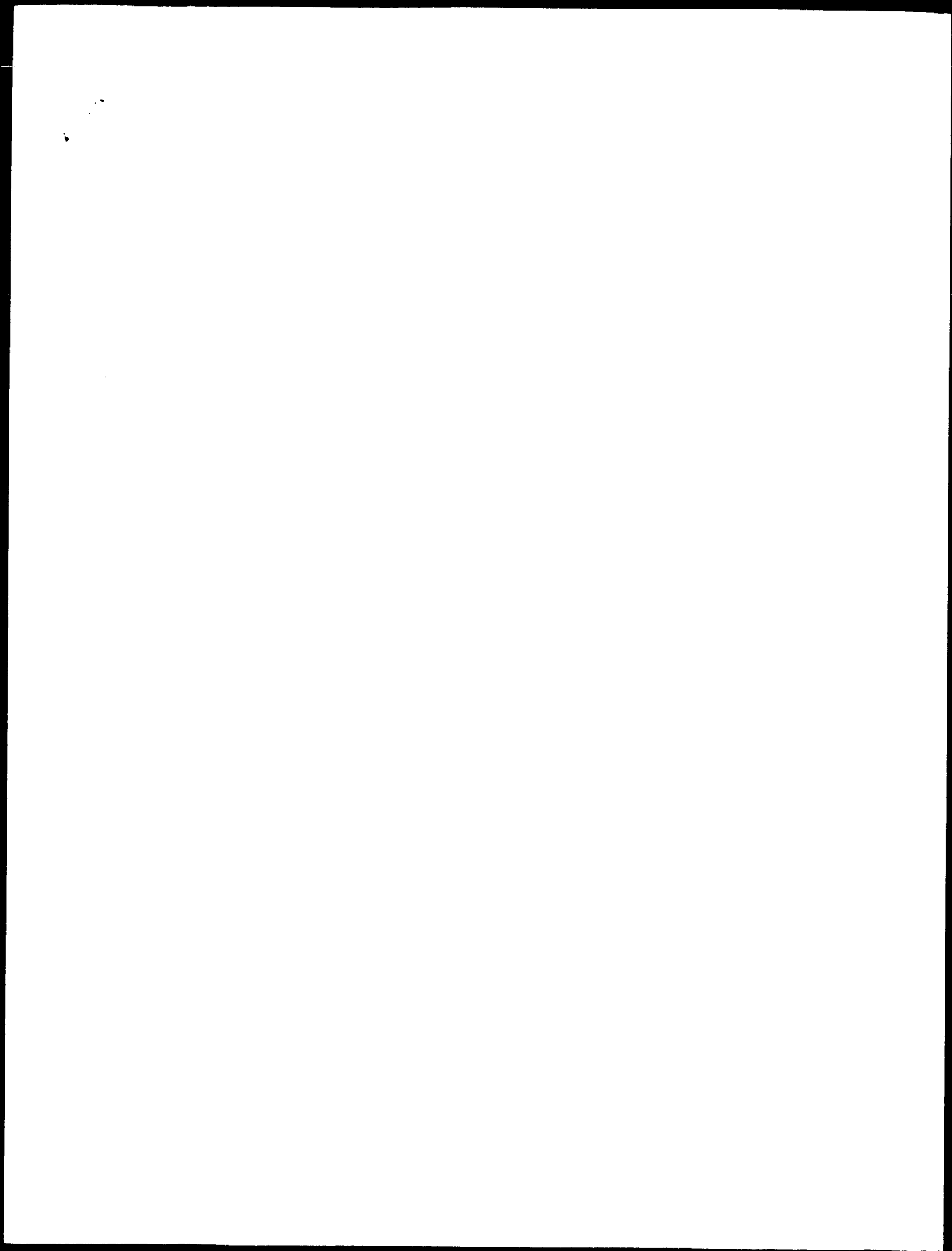
QY 1 FXXXW 5
DB 8 FATW 12

RESULT 15
US-09-240-203B-265
Sequence 265, Application US/09240203B
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
Pollock, Joanne;
Bond, Julian F.;
Garman, Richard D;
Kuo, Mei-Chang;
Powers, Steven P.;
Exley, Mark A.;
Chen, Xian;
Shaked, Zeev
TITLE OF INVENTION: Allergenic Proteins And Peptides From
Japanese Cedar Pollen
NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lanhive & Cockfield, LLP
STREET: 28 State St
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,203B
FILING DATE: 22-Jun-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras, Esq.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IM1-028CD2CCPA2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-240-203B-265

Query Match 85.0%; Score 17; DB 16; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.5e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0;
Gaps 0;
QY 1 FXXXW 5
1
1
DB 12 ESTAW 16

Search completed: January 29, 2003, 14:15:23
Job time : 139 secs



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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:11:42 ; Search time 18 Seconds
(without alignments)
21.950 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 396018 seqs, 79020188 residues

Total number of hits satisfying chosen parameters: 396018

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA-New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	85.0	41	5	US-09-966-264D-41 Sequence 41, Appl
2	17	85.0	44	6	US-10-203-138A-12357 Sequence 12357, A
3	17	85.0	46	6	US-10-203-138A-12178 Sequence 12178, A
4	17	85.0	51	1	PCT-US02-32727-19679 Sequence 19679, A
5	17	85.0	51	6	US-10-057-498-19679 Sequence 19679, A
6	17	85.0	52	1	PCT-US02-32727-17963 Sequence 17963, A
7	17	85.0	52	6	US-10-057-498-17963 Sequence 17963, A
8	17	85.0	54	5	US-09-733-643B-21 Sequence 21, Appl
9	17	85.0	56	1	PCT-US02-32727-25901 Sequence 25901, A
10	17	85.0	56	6	US-10-057-498-25901 Sequence 25901, A
11	17	85.0	58	1	PCT-US02-32727-8139 Sequence 8139, Ap
12	17	85.0	58	6	US-10-057-498-8139 Sequence 8139, A
13	17	85.0	60	1	PCT-US02-32727-26135 Sequence 26135, A
14	17	85.0	60	6	US-10-057-498-26135 Sequence 26135, A
15	17	85.0	61	1	PCT-US02-32727-7101 Sequence 7101, Ap
16	17	85.0	61	6	US-10-092-411A-4258 Sequence 4258, Ap
17	17	85.0	61	6	US-10-057-498-7101 Sequence 7101, Ap
18	17	85.0	63	1	PCT-US02-32727-3486 Sequence 3486, Ap
19	17	85.0	63	6	US-10-057-498-3486 Sequence 3486, Ap
20	17	85.0	67	1	PCT-US02-32727-3015 Sequence 3015, Ap
21	17	85.0	67	6	US-10-057-498-3015 Sequence 3015, Ap
22	17	85.0	68	1	PCT-US02-32727-4894 Sequence 4894, Ap
23	17	85.0	68	6	US-10-057-498-4894 Sequence 4894, A
24	17	85.0	69	1	PCT-US02-32727-13373 Sequence 13373, A
25	17	85.0	69	6	US-10-057-498-13373 Sequence 13373, A
26	17	85.0	71	1	PCT-US02-32727-8519 Sequence 8519, Ap

27	17	85.0	71	6	US-10-057-498-8519 Sequence 8519, Ap
28	17	85.0	72	1	PCT-US02-32727-9882 Sequence 9882, Ap
29	17	85.0	72	6	US-10-057-498-9882 Sequence 9882, Ap
30	17	85.0	74	1	PCT-US02-32727-16040 Sequence 16040, A
31	17	85.0	74	1	PCT-US02-32727-28942 Sequence 28942, A
32	17	85.0	74	6	US-10-057-498-16040 Sequence 16040, A
33	17	85.0	74	6	US-10-057-498-28942 Sequence 28942, A
34	17	85.0	76	1	PCT-US02-32727-848 Sequence 848, App
35	17	85.0	76	6	US-10-057-498-848 Sequence 848, App
36	17	85.0	76	6	US-10-057-498-848 Sequence 848, App
37	17	85.0	78	5	US-09-724-676A-63184 Sequence 63184, A
38	17	85.0	78	5	US-09-724-676A-63184 Sequence 63184, A
39	17	85.0	78	6	US-10-203-138A-10907 Sequence 10907, A
40	17	85.0	82	5	US-09-950-084-5109 Sequence 5109, Ap
41	17	85.0	83	6	US-10-218-140-866 Sequence 866, App
42	17	85.0	85	1	PCT-US02-32727-11518 Sequence 11518, A
43	17	85.0	85	6	US-10-057-498-11518 Sequence 11518, A
44	17	85.0	86	1	PCT-US02-32727-25616 Sequence 25616, A
45	17	85.0	86	6	US-10-057-498-25616 Sequence 25616, A

ALIGNMENTS

RESULT 1
US-09-966-264D-41
Sequence 41, Application US/09966264D
GENERAL INFORMATION:
APPLICANT: Barber, Elizabeth K
TITLE OF INVENTION: Gene Expression Control Element DNA
FILE REFERENCE: 896034605001
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 60/237,079
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
LENGTH: 41
TYPE: PRT
ORGANISM: human
US-09-966-264D-41

Query Match 85.0%; Score 17; DB 5; Length 41;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 2 FASW 6
RESULT 2
US-10-203-138A-12357
Sequence 12357, Application US/10203138A
GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: PB 0004 WO 8
CURRENT APPLICATION NUMBER: US/10/203,138A
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6

;; PRIOR FILING DATE: 03 October 2000 (03.10.00)
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 27 September 2000 (27.09.00)
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 21 September 2000 (21.09.00)
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 30 June 2000 (30.06.00)
;; NUMBER OF SEQ ID NOS: 15438
;; SOFTWARE: Molecular Dynamics Sequence Listing Engine
;; SEQ ID NO 12357
;; LENGTH: 44
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC004852.2
;; FEATURE:
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
;; FEATURE:
;; OTHER INFORMATION: EST_HUMAN HIT: AA320774.1, EVALUO 5.00e-10
;; FEATURE:
;; OTHER INFORMATION: SWISSPROT HIT: P11369, EVALUO 1.00e-03
US-10-203-138A-12357

Query Match 85.0%; Score 17; DB 6; Length 44;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 18 FAATW 22

RESULT 3
US-10-203-138A-12178
;; Sequence 12178, Application US/10203138A
;; GENERAL INFORMATION:
;; APPLICANT: Molecular Dynamics, Inc.
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: PB 0004 WO 8
;; CURRENT FILING DATE: 2002-08-02
;; PRIOR APPLICATION NUMBER: US/10/203,138A
;; PRIOR FILING DATE: 03 August 2000 (03.08.00)
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 04 February 2000 (04.02.00)
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 26 May 2000 (26.05.00)
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 03 August 2000 (03.08.00)
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 03 October 2000 (03.10.00)
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 27 September 2000 (27.09.00)
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 21 September 2000 (21.09.00)
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 30 June 2000 (30.06.00)
;; NUMBER OF SEQ ID NOS: 15438
;; SOFTWARE: Molecular Dynamics Sequence Listing Engine
;; SEQ ID NO 12178
;; LENGTH: 46
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC007938.1
;; FEATURE:
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.7
;; OTHER INFORMATION: EST_HUMAN HIT: BF642802.1, EVALUO 2.00e-19
;; FEATURE:

;; OTHER INFORMATION: SWISSPROT HIT: P53620, EVALUO 5.00e-15
US-10-203-138A-12178

Query Match 85.0%; Score 17; DB 6; Length 46;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 20 FAATW 24

RESULT 4
PCT-US02-32727-19679
;; Sequence 19679, Application PC/TUS0232727
;; GENERAL INFORMATION:
;; APPLICANT: Mitcham, Jennifer
;; APPLICANT: Skeiky, Yasir
;; APPLICANT: Persing, David
;; APPLICANT: Bhatia, Ajay
;; APPLICANT: Maisonneuve, Jean Francois
;; APPLICANT: Zhang, Yanni
;; APPLICANT: Jen, Shiyang
;; APPLICANT: Lodes, Michael
;; APPLICANT: Benson, Darin
;; APPLICANT: Jones, Robert
;; APPLICANT: Carter, Darlick
;; APPLICANT: Barth, Brenda
;; APPLICANT: Douglass, John
;; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
;; FILE REFERENCE: 210121.514C1
;; CURRENT APPLICATION NUMBER: PCT/US02/32727
;; CURRENT FILING DATE: 2002-10-11
;; NUMBER OF SEQ ID NOS: 30992
;; SEQ ID NO 19679
;; LENGTH: 51
;; TYPE: PRT
;; ORGANISM: Propionibacterium acnes
PCT-US02-32727-19679

Query Match 85.0%; Score 17; DB 1; Length 51;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 33 FASSW 37

RESULT 5
US-10-057-498-19679
;; Sequence 19679, Application US/10057498
;; GENERAL INFORMATION:
;; APPLICANT: Mitcham, Jennifer
;; APPLICANT: Skeiky, Yasir
;; APPLICANT: Persing, David
;; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
;; FILE REFERENCE: 210121.514
;; CURRENT APPLICATION NUMBER: US/10/057,498
;; CURRENT FILING DATE: 2001-04-20
;; NUMBER OF SEQ ID NOS: 29212
;; SEQ ID NO 19679
;; LENGTH: 51
;; TYPE: PRT
;; ORGANISM: Propionibacterium acnes
US-10-057-498-19679

Query Match 85.0%; Score 17; DB 6; Length 51;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 33 FASSW 37

RESULT 6

PCT-US02-32727-17963
 ; Sequence 17963, Application PC/US0232727
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitcham, Jennifer
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Persing, David
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Maisonneuve, Jean Francois
 ; APPLICANT: Zhang, Yanni
 ; APPLICANT: Wang, Siqing
 ; APPLICANT: Jen, Shylan
 ; APPLICANT: Lodes, Michael
 ; APPLICANT: Benson, Darin
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Barth, Brenda
 ; APPLICANT: Douglas, John
 ; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
 ; FILE REFERENCE: 210121.514C1
 ; CURRENT APPLICATION NUMBER: PCT/US02/32727
 ; CURRENT FILING DATE: 2002-10-11
 ; NUMBER OF SEQ ID NOS: 30992
 ; SEQ ID NO 17963
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Propionibacterium
 PCT-US02-32727-17963

Query Match 85.0%; Score 17; DB 1; Length 52;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 Db 8 FSSSW 12

RESULT 7

US-10-057-498-17963
 ; Sequence 17963, Application US/10057498
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitcham, Jennifer
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Persing, David
 ; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
 ; FILE REFERENCE: 210121.514
 ; CURRENT APPLICATION NUMBER: US/10/057,498
 ; CURRENT FILING DATE: 2001-04-20
 ; NUMBER OF SEQ ID NOS: 29212
 ; SEQ ID NO 17963
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Propionibacterium
 US-10-057-498-17963

Query Match 85.0%; Score 17; DB 6; Length 52;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 Db 8 FSSSW 12

RESULT 8

US-09-733-643B-21
 ; Sequence 21, Application US/09733643B
 ; GENERAL INFORMATION:

; APPLICANT: Laroche, Andre J.
 ; APPLICANT: Huang, Timothy Y
 ; APPLICANT: Lu, Zhen-Xiang
 ; APPLICANT: Frick, Michele M.
 ; APPLICANT: Huang, Hung Chang
 ; APPLICANT: Cheng, Kuo Joan
 ; TITLE OF INVENTION: Coniotyrium militans beta-(1,3) exoglucanase gene
 ; FILE REFERENCE: 24014US1
 ; CURRENT APPLICATION NUMBER: US/09/733,643B
 ; CURRENT FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: US 60/170,168
 ; PRIOR FILING DATE: 1999-12-12
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 21
 ; LENGTH: 54
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; OTHER INFORMATION: Exopg
 US-09-733-643B-21

Query Match 85.0%; Score 17; DB 5; Length 54;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 Db 23 FAAMW 27

RESULT 9

PCT-US02-32727-25901
 ; Sequence 25901, Application PC/US0232727
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitcham, Jennifer
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Persing, David
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Maisonneuve, Jean Francois
 ; APPLICANT: Zhang, Yanni
 ; APPLICANT: Wang, Siqing
 ; APPLICANT: Jen, Shylan
 ; APPLICANT: Lodes, Michael
 ; APPLICANT: Benson, Darin
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Barth, Brenda
 ; APPLICANT: Douglas, John
 ; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
 ; FILE REFERENCE: 210121.514C1
 ; CURRENT APPLICATION NUMBER: PCT/US02/32727
 ; CURRENT FILING DATE: 2002-10-11
 ; NUMBER OF SEQ ID NOS: 30992
 ; SEQ ID NO 25901
 ; LENGTH: 56
 ; TYPE: PRT
 ; ORGANISM: Propionibacterium
 PCT-US02-32727-25901

Query Match 85.0%; Score 17; DB 1; Length 56;
 Best Local Similarity 40.0%; Pred. No. 2.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 Db 45 FTSTW 49

RESULT 10

US-10-057-498-25901
 ; Sequence 25901, Application US/10057498

```
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 25901
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-25901
```

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Query Match      85.0%; Score 17; DB 6; Length 56;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 FXXXW 5
| 1
| 1
Dt 45 FSTTW 49
```

```
RESULT 11
PCT-US02-32727-8139
; Sequence 8139, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglas, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514cl
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 8139
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-8139
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```
Query Match      85.0%; Score 17; DB 1; Length 58;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 FXXXW 5
| 1
| 1
Db 45 FATSW 49
```

```
RESULT 12
US-10-057-498-8139
; Sequence 8139, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
```

```
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 8139
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-8139
```

```
Query Match      85.0%; Score 17; DB 6; Length 58;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 FXXXW 5
| 1
| 1
Db 45 FATSW 49
```

```
RESULT 13
PCT-US02-32727-26135
; Sequence 26135, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglas, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514cl
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 26135
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-26135
```

```
Query Match      85.0%; Score 17; DB 1; Length 60;
Best Local Similarity 40.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 FXXXW 5
| 1
| 1
Db 34 FSTTW 38
```

```
RESULT 14
US-10-057-498-26135
; Sequence 26135, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 26135
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-26135
```

```
Query Match      85.0%; Score 17; DB 6; Length 60;
```

Best Local Similarity 40.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXW 5
| |
Db 34 FSTW 38

RESULT 15
PCT-US02-32727-7101

; Sequence 7101, Application PC/TUS0232727
; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David

; APPLICANT: Bhatia, Ajay

; APPLICANT: Maisonneuve, Jean Francois

; APPLICANT: Zhang, Yanni

; APPLICANT: Wang, Sigling

; APPLICANT: Jen, Shyian

; APPLICANT: Lodes, Michael

; APPLICANT: Benson, Darin

; APPLICANT: Jones, Robert

; APPLICANT: Carter, Darlick

; APPLICANT: Barth, Brenda

; APPLICANT: Douglass, John

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes V

; FILE REFERENCE: 210121.514C1

; CURRENT APPLICATION NUMBER: PCT/US02/32727

; CURRENT FILING DATE: 2002-10-11

; NUMBER OF SEQ ID NOS: 30992

; SEQ ID NO 7101

; LENGTH: 61

; TYPE: PRT

; ORGANISM: Propionibacterium acnes

PCT-US02-32727-7101

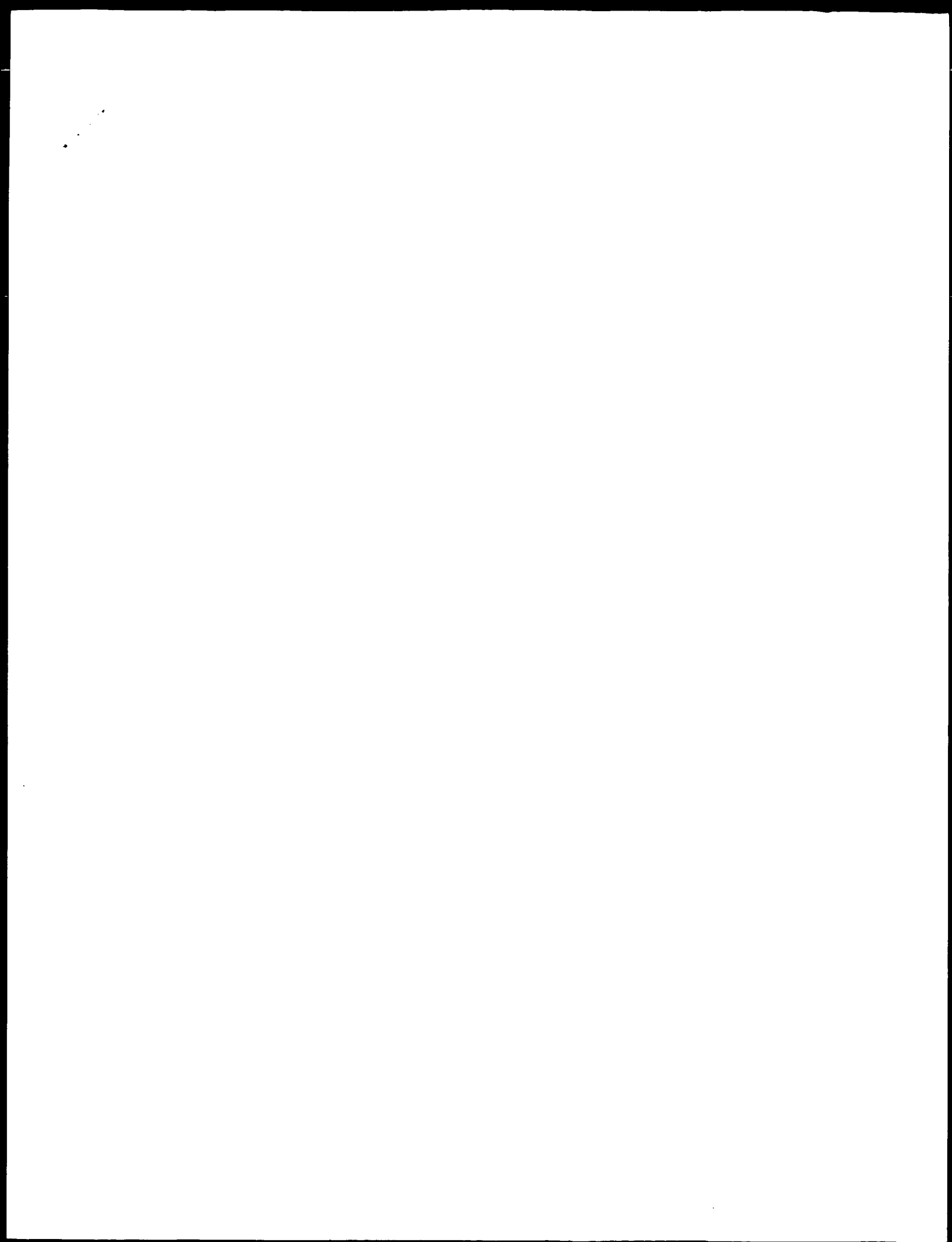
Query Match

Best Local Similarity 40.0%; Score 17; DB 1; Length 61;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXW 5
| |
Db 22 FSSW 26

Search completed: January 29, 2003, 14:15:47
Job time : 18 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:10:42 : Search time 15 Seconds
(without alignments)

9.808 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20

Sequence: 1 FXXXW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	85.0	13	4	US-09-085-072-7
2	17	85.0	29	4	US-08-469-260A-478
3	17	85.0	34	1	US-08-118-270-134
4	17	85.0	34	1	US-08-118-270-172
5	17	85.0	34	5	PCT-US93-08528-134
6	17	85.0	34	5	PCT-US93-08528-134
7	17	85.0	36	3	US-08-467-023-137
8	17	85.0	37	4	US-09-330-914A-10
9	17	85.0	41	3	US-08-467-023-135
10	17	85.0	45	3	US-08-467-023-135
11	17	85.0	45	4	US-09-149-476-475
12	17	85.0	49	1	US-08-118-270-209
13	17	85.0	49	5	PCT-US93-08528-209
14	17	85.0	61	4	US-09-134-001C-4258
15	17	85.0	80	4	US-09-330-914A-4
16	17	85.0	84	2	US-08-353-476-78
17	17	85.0	84	4	US-08-679-493A-97
18	17	85.0	91	2	US-08-598-873-19
19	17	85.0	91	4	US-08-605-430-19
20	17	85.0	102	3	US-08-984-295-3
21	17	85.0	102	3	US-08-741-411-12
22	17	85.0	104	6	5210073-1
23	17	85.0	105	2	US-08-826-910-3
24	17	85.0	105	2	US-08-826-910-4
25	17	85.0	114	4	US-09-450-520A-9
26	17	85.0	114	4	US-09-450-520A-10
27	17	85.0	114	4	US-09-450-520A-11

28	17	85.0	116	3	US-09-065-059-9	Sequence 9, Appl
29	17	85.0	116	3	US-08-545-809A-134	Sequence 134, App
30	17	85.0	117	1	US-07-634-278-105	Sequence 105, App
31	17	85.0	117	1	US-08-477-728-105	Sequence 105, App
32	17	85.0	117	1	US-08-474-040-105	Sequence 105, App
33	17	85.0	117	1	US-08-487-200-105	Sequence 105, App
34	17	85.0	117	4	US-08-484-537-105	Sequence 105, App
35	17	85.0	120	3	US-09-065-059-1	Sequence 1, Appl
36	17	85.0	122	4	US-09-540-014-2	Sequence 2, Appl
37	17	85.0	127	4	US-09-540-014-4	Sequence 4, Appl
38	17	85.0	128	3	US-08-467-023-187	Sequence 187, App
39	17	85.0	130	1	US-08-276-852-69	Sequence 69, App
40	17	85.0	130	1	US-08-276-852-70	Sequence 70, Appl
41	17	85.0	130	1	US-08-276-852-71	Sequence 71, Appl
42	17	85.0	130	1	US-08-899-575-69	Sequence 69, Appl
43	17	85.0	130	1	US-08-899-575-70	Sequence 70, Appl
44	17	85.0	130	1	US-08-899-575-71	Sequence 71, Appl
45	17	85.0	130	1	US-08-899-575-69	Sequence 69, Appl

ALIGNMENTS

RESULT 1
US-09-085-072-7
Sequence 7, Application US/09085072
Patent No. 6265150
GENERAL INFORMATION:
APPLICANT: L. Terstappen et al.
TITLE OF INVENTION: PHAGE ANTIBODIES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: USA
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,072
FILING DATE: 26-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: 890-2 FWC/CLP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-085-072-7

Query Match 85.0% Score 17: DB 4: Length 13:
Best Local Similarity 40.0% Pred. No. 8.7e+02:
Matches 2: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

QY 1 FXXXW 5
DB 6 FASSW 10

RESULT 2

US-08-469-260A-428
Sequence 428, Application US/08469260A
Patent No. 6451578
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMT J. PILOT-MARTIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHRHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIKAR
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 428:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-260A-428

Query Match 85.0%; Score 17; DB 4; Length 29;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 12 FASAW 16

RESULT 3
US-08-118-270-134
Sequence 134, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-134

Query Match 85.0%; Score 17; DB 1; Length 34;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 16 FTSAW 20

RESULT 4
US-08-118-270-172
Sequence 172, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-172

Query Match 85.0%; Score 17; DB 1; Length 34;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 16 FTTAW 20

RESULT 5
PCT-US93-08528-134
Sequence 134, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-134

Query Match 85.0%; Score 17; DB 5; Length 34;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 16 FTTAW 20

RESULT 6
PCT-US93-08528-172
Sequence 172, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-172

Query Match 85.0%; Score 17; DB 5; Length 34;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 16 FTTAW 20

RESULT 7
US-08-467-023-137
Sequence 137, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St

CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-467-023-137

Query Match 85.0%; Score 17; DB 3; Length 36;
Best Local Similarity 40.0%; Pred No. 1.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 28 FSTAW 32

RESULT 8
US-09-330-914A-10
Sequence 10, Application US/09330914A
Patent No. 6432671
GENERAL INFORMATION:
APPLICANT: Flohe, Leopold
No. 6432671ecke, Everson
Kalisz, Henryk
Montemartini, Marisa
TITLE OF INVENTION: TRYPARDOXIN, EXPRESSION PLASMID, PROCESS OF
PRODUCTION, METHOD OF USE, TEST KIT, AND
PHARMACEUTICAL COMPOSITION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Brown
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,914A
FILING DATE: 11-Jun-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP97/06983
FILING DATE: 12-DEC-1997

ATTORNEY/AGENT INFORMATION:
NAME: Zeller, James P.
REGISTRATION NUMBER: 28,491
REFERENCE/DOCKET NUMBER: 29473/35678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-330-914A-10

Query Match 85.0%; Score 17; DB 4; Length 37;
Best Local Similarity 40.0%; Pred No. 1.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 11 FSASW 15

RESULT 9
US-08-467-023-136
Sequence 136, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Giffeth, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:

LENGTH: 41 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-467-023-136

Query Match 85.0%; Score 17; DB 3; Length 41;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 33 FSTW 37

RESULT 10
US-08-467-023-135
Sequence 135, Application US/08467023
Patent No. 6090386

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF INVENTION: Japanese Cedar Pollen
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard

REGISTRATION NUMBER:

REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 US02 (IM1-028CPD2)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ. ID NO. 135:

SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-467-023-135

Query Match 85.0%; Score 17; DB 3; Length 45;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5

DB 33 FSTW 37

RESULT 11

US-09-149-476-475
Sequence 475, Application US/09149476
Patent No. 6420526

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERENCE: P2002P1

CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601

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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043, 580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043, 568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043, 314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043, 569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043, 311
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; EARLIER APPLICATION NUMBER: 60/043, 671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043, 674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043, 669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043, 312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043, 313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043, 672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043, 315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048, 974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056, 886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 892
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/057, 761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047, 595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047, 599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047, 588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047, 585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047, 586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047, 590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047, 594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047, 589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047, 593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047, 614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043, 578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043, 576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047, 501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043, 670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056, 632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056, 908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048, 964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057, 650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056, 884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057, 669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049, 610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061, 060
; EARLIER FILING DATE: 1997-10-02

Query Match      85.0%; Score 17; DB 4; Length 45;
Best Local Similarity 40.0%; Pred. No. 2, 1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      1 FXXW 5
DB      31 FSAW 35

RESULT 12
US-08-118-270-209
; Sequence 209, Application US/08118270
```

Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-209

Query Match 85.0%; Score 17; DB 1; Length 49;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 36 FTSW 40

RESULT 13
PCT-US93-08528-209
Sequence 209, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-209

Query Match 85.0%; Score 17; DB 5; Length 49;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 36 FTSW 40

RESULT 14
US-09-134-001C-4258
Sequence 4258, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4258
LENGTH: 61
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4258

Query Match 85.0%; Score 17; DB 4; Length 61;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 14 FTSW 18

RESULT 15
US-09-330-914A-4
Sequence 4, Application US/09330914A
Patent No. 6432671
GENERAL INFORMATION:
APPLICANT: Flohe, Leopold
No. 6432671e4e4e, Everson
Kallisz, Henryk
Montemattini, Marisa
TITLE OF INVENTION: TRYPAEDOXIN, EXPRESSION PLASMID, PROCESS OF
PRODUCTION, METHOD OF USE, TEST KIT, AND
PHARMACEUTICAL COMPOSITION

```

:      NUMBER OF SEQUENCES: 15
:      CORRESPONDENCE ADDRESS:
:      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Brown
:      STREET: 233 South Wacker Drive/6300 Sears Tower
:      CITY: Chicago
:      STATE: Illinois
:      COUNTRY: United States of America
:      ZIP: 60606
:
:      COMPUTER READABLE FORM:
:      MEDIUM TYPE: floppy disk
:      COMPUTER: IBM PC compatible
:      OPERATING SYSTEM: PC-DOS/MS-DOS
:      SOFTWARE: Patent In Release #1.0, Version #1.30
:
:      CURRENT APPLICATION DATA:
:      APPLICATION NUMBER: US/09/330,914A
:      FILING DATE: 11-Jun-1999
:      CLASSIFICATION: <unknown>
:
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: WO PCT/EP97/06983
:      FILING DATE: 12-DEC-1997
:
:      ATTORNEY/AGENT INFORMATION:
:      NAME: Zeller, James P.
:      REGISTRATION NUMBER: 28,491
:      REFERENCE/DOCKET NUMBER: 29473/35678
:      TELECOMMUNICATION INFORMATION:
:      TELEPHONE: (312) 474-6300
:      TELEFAX: (312) 474-0448
:
:      INFORMATION FOR SEQ ID NO: 4:
:      SEQUENCE CHARACTERISTICS:
:      LENGTH: 80 amino acids
:      TYPE: amino acid
:      STRANDEDNESS: single
:      TOPOLOGY: linear
:      MOLECULE TYPE: protein
:      HYPOTHETICAL: NO
:      ANTI-SENSE: NO
:
:      SEQUENCE DESCRIPTION: SEQ ID NO: 4:
:
:      US-09-330-914A-4
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:      Query Match      85.0%; Score 17; DB 4; Length 80;
:      Best Local Similarity 40.0%; Pred. No. 3.1e+03;
:      Matches 2; Conservative 0; Mismatches 3; Indels 0;
:
:      QY      1 FXXXW 5
:      Db      8 FSASW 12

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Search completed: January 29, 2003, 14:12:57
 Job time : 16 secs

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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:15:53 : Search time 15 Seconds
(without alignments)
32.045 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	85.0	9	2	A24244 adipokineic hormo
2	16	80.0	8	2	A28004 adipokineic hormo
3	16	80.0	10	2	A31571 hypertrehalosemic/
4	15	75.0	8	2	S10596 adipokineic hormo
5	15	75.0	9	2	D57444 neuropeptide Grb-A
6	15	75.0	10	2	T17063 cytochrome-c oxida
7	15	75.0	10	2	T12325 cytochrome-c oxida
8	15	75.0	10	2	S53789 neuropeptide Pec-H
9	15	75.0	15	2	PH1613 Ig H chain V-D-J r
10	15	75.0	17	2	A34704 protein-tyrosine k
11	15	75.0	20	2	S77981 cytochrome-c oxida
12	15	75.0	20	2	PN0171 peptidylprolyl iso
13	15	75.0	20	2	PH1380 alpha-amylase (EC
14	14	70.0	8	2	A61348 red pigment-concen
15	14	70.0	8	2	S08995 hypertrehalosemic
16	14	70.0	8	2	S08996 hypertrehalosemic
17	14	70.0	8	2	A49823 adipokineic hormo
18	14	70.0	8	2	A49823 adipokineic hormo
19	14	70.0	8	2	A44960 neuropeptide Led-C
20	14	70.0	8	2	B44960 neuropeptide Led-C
21	14	70.0	8	2	A43976 hypertrehalosemic
22	14	70.0	8	2	B43976 hypertrehalosemic
23	14	70.0	8	2	A33995 adipokineic hormo
24	14	70.0	8	2	S11545 adipokineic hormo
25	14	70.0	8	2	S5310 adipokineic hormo
26	14	70.0	8	2	A58620 adipokineic hormo
27	14	70.0	8	2	A05169 neuropeptide M-I -
28	14	70.0	10	2	A60421 hypertrehalosemic
29	14	70.0	10	2	S08997 hypertrehalosemic

30	14	70.0	10	2	S08998 hypertrehalosemic
31	14	70.0	10	2	A26381 hypertrehalosemic
32	14	70.0	10	2	JC1416 hypertrehalosemic
33	14	70.0	10	2	S09138 hypertrehalosemic
34	14	70.0	10	2	B33995 hypertrehalosemic
35	14	70.0	10	2	C39191 hypothetical prote
36	14	70.0	10	2	PF0322 Ig heavy chain CRD
37	14	70.0	10	2	T17066 cytochrome-c oxida
38	14	70.0	10	2	T17069 cytochrome-c oxida
39	14	70.0	10	2	T12329 Ig heavy chain CRD
40	14	70.0	12	2	PT0274 Ig heavy chain DJ
41	14	70.0	12	2	PH1324 cysteine proteinase
42	14	70.0	13	2	PC4391 homeotic protein G
43	14	70.0	16	2	C37290 nitrogen fixation
44	14	70.0	19	2	S32675 calcium-binding pr
45	14	70.0	20	2	PC1240

ALIGNMENTS

RESULT 1
A24244
adipokineic hormone - bollworm
N:Alternate names: Hez-AKH
C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C:Date: 31-Mar-1988 #sequence...
C:Accession: ...

T.: Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridg
, 622-628, 1986
icture of a peptide from the corpora cardiaca of He
1186794; PMID:3964263

Seq length
= 20

orpora cardiaca; hormone; neuropeptide; pyrogluta
xylic acid (Gln) #status experimental
end (Gly) #status experimental

I
QY 1 FXXXW 5
Db 4 FTSSW 8
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 2
A28004
adipokineic hormone G - two-spotted cricket

N:Alternate names: AKH-G
C:Species: Gryllus bimaculatus (two-spotted cricket)
C:Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 24-Oct-1997

R:saede, G.; Rinehart, K.L.
Biochem. Biophys. Res. Commun. 149, 908-914, 1987

A:Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a pe
A:Reference number: A28004; MUID:88106553; PMID:342616

A:Accession: A28004
A:Molecule type: protein

A:Residues: 1-8 <CAE>
A:Note: The amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we h
A:Superfamily: adipokineic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 80.0%; Score 16; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
|
|
Db 4 FSTGW 8

RESULT 3

A11571
hypertrahalosemic/adipokinetic hormone - bollworm
N:Alternate names: Hez-HrTH
C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C>Date: 30-Jun-1989 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C:Accession: A11571
R:Jaffe, H.; Raine, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S.
Biochem. Biophys. Res. Commun. 155, 344-350, 1988
A:Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea w
A:Reference number: A11571; MUID:88326324; PMID:3415690
A:Accession: A11571
A:Molecule type: protein
A:Residues: 1-10 <JAF>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 80.0%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
|
|
Db 4 FSTGW 8

RESULT 4

S10596
adipokinetic hormone - pond skimmer
C:Species: Libellula auripennis
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 14-Nov-1997
C:Accession: S10596
R:Gaede, G.
Biol. Chem. Hoppe-Seyler 371, 475-483, 1990
A:Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating ho
A:Reference number: S10596; MUID:90359055; PMID:2390213
A:Accession: S10596
A:Molecule type: protein
A:Residues: 1-8 <BIO>
C:Comment: This peptide has both adipokinetic and hypertrahalosemic activities.
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 75.0%; Score 15; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
|
|
Db 4 FSTGW 8

RESULT 5

D57444
neuropeptide Grp-AST B4 - two-spotted cricket
C:Species: Gryllus bimaculatus (two-spotted cricket)
C>Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C:Accession: D57444
R:Jorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cri
A:Reference number: A57444; MUID:95403341; PMID:7673141
A:Accession: D57444
A:Status: preliminary

A:Molecule type: protein
A:Residues: 1-9 <LOR>

Query Match 75.0%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
|
|
Db 5 FHGSW 9

RESULT 6

T17063
cytochrome-c oxidase (EC 1.9.3.1) chain I - Haploecercus spinosus mitochondrion (fragm
C:Species: mitochondrion Haploecercus spinosus
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C:Accession: T17063
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A:Title: Evolutionary shifts in three major structural features of the mitochondrial
A:Reference number: T17063; MUID:97315309; PMID:9165559
A:Accession: T17063
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <MAC>
A:Cross-references: EMBL:U82683; NID:93603124; PTD:93603127; PIDN:AAC62284.1
C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 75.0%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
|
|
Db 2 FISRW 6

RESULT 7

T12325
cytochrome-c oxidase (EC 1.9.3.1) chain I - Leloecephalus carinatus mitochondrion (fra
C:Species: mitochondrion Leloecephalus carinatus
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999
C:Accession: T12325
R:Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A:Title: Molecular tests of phylogenetic taxonomies: A general procedure and example
A:Reference number: T12325; MUID:99162288; PMID:10051389
A:Accession: T12325
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <SCH>
A:Cross-references: EMBL:AF049864; NID:94105754; PTD:94105757; PIDN:AAD02535.1
C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 75.0%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
|
|
Db 2 FITRW 6

RESULT 8

S53789
neuropeptide Pec-HrTH - Platypleura capensis

C:Species: *Platypleura capensis*
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
 C:Accession: S53789
 R:Gaede, G.; Janssens, M.P.E.
 B:Jol. Chem. Hoppe-Seyler 375, 803-809, 1994
 A:Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehalose
 A:Reference number: S53789; MUID:95225985; PMID:7710694
 A:Accession: S53789
 A:Molecule type: protein
 A:Residues: 1-10 <GAE>
 C:Keywords: blocked amino end; blocked carboxyl end

Query Match 75.0%; Score 15; DB 2; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 | |
 DB 4 FSPSW 8

RESULT 9
 PH1613
 Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)
 C:Species: *Mus musculus* (house mouse)
 C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1613
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 176, 317-329, 1993
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1580; MUID:93301609; PMID:8315387
 A:Accession: PH1613
 A:Molecule type: DNA
 A:Residues: 1-15 <LEF>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Query Match 75.0%; Score 15; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 1.6e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 | |
 DB 10 FTMLM 14

RESULT 10
 A34704
 protein-tyrosine kinase (EC 2.7.1.112) 1, neuron-specific - human (fragment)
 C:Species: *Homo sapiens* (man)
 C:Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 04-Feb-2000
 C:Accession: A34704
 R:Pyper, J.M.; Bolen, J.B.
 Mol. Cell. Biol. 10, 2035-2040, 1990
 A:Title: Identification of a novel neuronal C-SRC exon expressed in human brain.
 A:Reference number: A34704; MUID:90220588; PMID:1691439
 A:Accession: A34704
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-17 <PVP>
 C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 75.0%; Score 15; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 1.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 | |
 DB 10 FTFRW 14

RESULT 11
 S7981

cytochrome-c oxidase (EC 1.9.3.1) chain Va.1 - bigeye tuna (fragment)
 C:Species: *Thunnus obesus* (bigeye tuna)
 C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 26-Feb-1998
 C:Accession: S7981
 R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
 Submitted to the Protein Sequence Database, June 1997
 A:Reference number: S7980
 A:Accession: S7981
 A:Molecule type: protein
 A:Residues: 1-20 <ARN>
 A:Experimental source: heart; liver
 C:Genetics:
 A:Genome: nuclear
 C:Function:
 A:Pathway: oxidative phosphorylation; respiratory chain
 C:Superfamily: mammalian cytochrome-c oxidase chain Va
 C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membr

Query Match 75.0%; Score 15; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 1.9e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 | |
 DB 11 FDKRW 15

RESULT 12
 PN0171
 peptidylprolyl isomerase (EC 5.2.1.8) b, cytosolic - fungus (*Fusarium sporotrichoides*
 N:Contains: cyclophilin
 C:Species: *Fusarium sporotrichoides*
 C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 02-Sep-2000
 C:Accession: PN0171
 R:Fukaya, N.; Chow, L.P.; Sugitara, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
 Submitted to JPIPD, May 1994
 A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichoides*
 A:Reference number: PN0160
 A:Accession: PN0171
 A:Molecule type: protein
 A:Residues: 1-20 <FKU>
 A:Experimental source: strain M-1-1
 A:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; cytosol

Query Match 75.0%; Score 15; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 1.9e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
 | |
 DB 6 FDIW 10

RESULT 13
 PH1380
 alpha-amylose (EC 3.2.1.1) (Halm sensitive) - *Bacillus* sp. (fragment)
 C:Species: *Bacillus* sp.
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 07-May-1999
 C:Accession: PH1380
 R:Kawaguchi, T.; Nagae, H.; Murao, S.; Arai, M.
 Biosci. Biotechnol. Biochem. 56, 1792-1796, 1992
 A:Title: Purification and some properties of a Halm-sensitive alpha-amylose from new
 A:Reference number: PH1380; MUID:93113087; PMID:1369074
 A:Accession: PH1380
 A:Molecule type: protein
 A:Residues: 1-20 <KAW>
 A:Experimental source: strain NO.195
 C:Comment: This enzyme has an optimum pH of 7.0.
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 75.0%; Score 15; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 1.9e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
 | |
 Db 13 FSWTW 17

RESULT 14

A61348
 red pigment-concentrating hormone - northern shrimp
 N:Alternate names: blanching hormone
 C:Species: *Pandalus borealis* (northern shrimp)
 C>Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
 C:Accession: A61348; S07139
 R:Fernlund, P.; Josefsson, L.
 Science 177, 173-175, 1972
 A>Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
 A:Reference number: A61348; MUID:7228738; PMID:5041363
 A:Accession: A61348
 A:Molecule type: protein
 A:Residues: 1-8 <FERI>
 R:Fernlund, P.
 Biochim. Biophys. Acta 371, 304-311, 1974
 A>Title: Structure of the red-pigment-concentrating hormone of the shrimp, *Pandalus borealis*.
 A:Reference number: S07139; MUID:75054965; PMID:4433569
 A:Accession: S07139
 A:Molecule type: protein
 A:Residues: 'E', 2-8 <FER2>
 A>Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have zed pigment-containing cells.
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamate
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 70.0%; Score 14; DB 2; Length 8;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
 | |
 Db 4 FSPGW 8

RESULT 15

S03995
 hypertrehalosemic hormone I - oriental cockroach
 N:Alternate names: Pea-CAH-I
 C:Species: *Blattella orientalis* (oriental cockroach)
 C>Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
 C:Accession: S08995
 R:Saede, G.; Rinehart, K.L.
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
 A>Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bombardment
 A:Reference number: S08995; MUID:90253659; PMID:2340112
 A:Accession: S08995
 A:Molecule type: protein
 A:Residues: 1-8 <GAE>
 A>Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 70.0%; Score 14; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
 | |
 Db 4 FSPNW 8

Search completed: January 29, 2003, 14:17:59
 Job time: 15 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:13:03 ; Search time 10 seconds
(without alignments)
20.738 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20
Sequence: 1 FXXW 5

Scoring table: BIOSUM62
Gapop 10.0, Capext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1147

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	16	80.0	8	AKHG_GRYBI	P14086 gryllus bim
2	16	80.0	10	HTF_HELZE	P16353 heliothis z
3	15	75.0	8	AKH_LIBAU	P23418 libellula a
4	15	75.0	10	AKHX_LOCM1	P81626 locusta mlg
5	15	75.0	20	COXA_THUOB	P80972 thunnus obe
6	14	70.0	8	AKH_TABAT	P14595 tabanus atr
7	14	70.0	8	HTF1_PERAM	P04548 periplaneta
8	14	70.0	8	HTF2_PERAM	P25419 tenebrio mo
9	14	70.0	8	HTF_TEMMO	P08939 pandanus bo
10	14	70.0	10	RPCH_PANBO	P18110 romalea mlc
11	14	70.0	10	HTF1_ROMMI	P11385 carausius m
12	14	70.0	10	HTF2_CARMO	P10939 nauphoeta c
13	14	70.0	10	HTF_NAUCI	P14596 tabanus atr
14	14	70.0	10	HTF_TABAT	P04548 periplaneta
15	14	70.0	13	YPNP_PPHOLU	P25419 tenebrio mo
16	14	70.0	20	CRTC_SPIOL	P30806 spinacia ol
17	13	65.0	6	ETI01_LITRU	P84296 litorea rub
18	12	60.0	10	GONI_PETMA	P04378 petromyzon
19	12	60.0	11	CA31_LITCI	P82089 litorea cit
20	12	60.0	11	CA32_LITCI	P82090 litorea cit
21	12	60.0	11	COR2_PERAM	P11496 periplaneta
22	11	55.0	4	OCIP3_OCCMI	P58649 octopius min
23	11	55.0	5	BP7_BOTIN	P30425 bothrops in
24	11	55.0	5	UF01_MOUSE	P38639 mus musculu
25	11	55.0	6	LOK1_LOCM1	P41491 locusta mlg
26	11	55.0	7	BRHP_CONIM	P58803 conus imper
27	11	55.0	7	TY51_LITRU	P82065 litorea rub
28	11	55.0	7	WWA1_ACHFU	P35919 achetina fu
29	11	55.0	7	WWA2_ACHFU	P35920 achetina fu
30	11	55.0	7	WMA3_ACHFU	P35921 achetina fu
31	11	55.0	8	ACT_THUAL	P18691 thunnus alb
32	11	55.0	8	AKH_MEIHL	P25423 melolontha
33	11	55.0	8	CCKN_MACEU	P30369 macropus eu

34	11	55.0	8	1	COW2_CONPU	P58785 conus purpu
35	11	55.0	8	1	LCK1_LEUMA	P21140 leucophaea
36	11	55.0	8	1	LCK2_LEUMA	P21141 leucophaea
37	11	55.0	8	1	LCK3_LEUMA	P21142 leucophaea
38	11	55.0	8	1	LCK4_LEUMA	P21143 leucophaea
39	11	55.0	8	1	LCK5_LEUMA	P19987 leucophaea
40	11	55.0	8	1	LCK6_LEUMA	P19988 leucophaea
41	11	55.0	8	1	LCK7_LEUMA	P19989 leucophaea
42	11	55.0	8	1	LCK8_LEUMA	P19990 leucophaea
43	11	55.0	8	1	PLP_BRANA	P81707 brassica na
44	11	55.0	9	1	COW_CONVE	P83047 conus ventr
45	11	55.0	9	1	DL_NEPNO	P24816 nephtrops no

ALIGNMENTS

RESULT 1
AKHG_GRYBI STANDARD: PRT: 8 AA.

AC P14086:
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Adipokinetic hormone (Two-spotted cricket), and
OS Gryllus bimaculatus (lubber grasshopper).
OC Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera;
OC Gryllidae; Gryllinae; Gryllus.
OX NCBI_TaxID=6959, 7007;

RN (1)
RP SEQUENCE:
RC SPECIES=G. bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.:
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
of a peptide with adipokinetic activity from the corpora cardiaca of
the cricket Gryllus bimaculatus."
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).

RN [2]
RP SEQUENCE:
RC SPECIES=R. microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Rinehart K.L. Jr.:
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
the lubber grasshopper, Romalea microptera."
RL Peptides 9:681-688(1988).
CC -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -I- SIMILARITY: BELONGS TO THE AKH / RHTH / RPCH FAMILY.
DR PIR: A28004; A28004.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA: 938 MW: 86786185B9C452D6 CRC64;

Query Match 80.0%; Score 16; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 4 FSTGW 8

RESULT 2
HTF_HELZE STANDARD: PRT: 10 AA.
ID HTF_HELZE

AC P16353;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hyperthrealeosmic hormone (Hez-HRH).
 OS Heliothis zea (Corn earworm) (Bollworm).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 CC Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Helioverpa.
 NCBI_TaxID=7113;
 [1]

R2 SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=88326324; PubMed=3415690;
 RA Tseff H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
 RA Tseng C.M., Zhang Y.S., Hayes D.K.;
 RT "Isolation and primary structure of a neuropeptide hormone from
 RT Heliothis zea with hyperthrealeosmic and adipokinetic activities."
 RL Biochem. Biophys. Res. Commun. 155:344-350(1988).
 CC -1- FUNCTION: HYPERTHREALEOSMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYPH OF INSECTS).
 DR PIR: A31571; A31571.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1
 FT MOD_RES 10 10
 SC SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

Query Match 80.0%; Score 16; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 2.9e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXX 5
 DB 4 FSSGW 8

RESULT 3
 AKH LIBAU
 ID AKH LIBAU STANDARD; PRT; 8 AA.
 AC P25418;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Adipokinetic hormone (AKH).
 OS Libellula auripennis (Skimmer dragonfly).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Palaeoptera; Odonata; Anisoptera; Libellulidae;
 CC Libellula.
 NCBI_TaxID=65966;
 [1]
 RN RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90359055; PubMed=2390213;
 RA Gaede G.;
 RT "The putative ancestral peptide of the adipokinetic/red-pigment-
 RT concentrating hormone family isolated and sequenced from a
 RT dragonfly."
 RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
 CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight.
 FT MOD_RES 1 1
 FT MOD_RES 8 8
 CC SEQUENCE, AND SYNTHESIS.
 CC PIR: S10596; S10596.
 CC InterPro: IPR002047; AKH.
 CC PROSITE: PS00256; AKH; 1.
 CC MOD_RES 1 1
 CC MOD_RES 8 8
 CC PIRROLIDONE CARBOXYLIC ACID.
 CC AMIDATION.

SO SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 75.0%; Score 15; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXX 5
 DB 4 FTFSW 8

RESULT 4
 AKHX LOCMI
 ID AKHX LOCMI STANDARD; PRT; 10 AA.
 AC P81626;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peptide hormone.
 OS Locusta migratoria (Migratory locust).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.
 NCBI_TaxID=7004;
 [1]
 RN RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RA Siebert K.T.;
 RL Submitted (DEC-1998) to the SWISS-PROT data bank.
 CC -1- FUNCTION: PROBABLY INVOLVED IN THE REGULATION OF LOCUST
 CC INTERMEDIARY METABOLISM, BEHAVIOR AND/OR DEVELOPMENT.
 CC -1- SIMILARITY: SOME SIMILARITY TO THE AKH / HRTH / RPCH FAMILY.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1
 FT MOD_RES 10 10
 SC SEQUENCE 10 AA; 1222 MW; 81BFF67AB415B9D1 CRC64;

Query Match 75.0%; Score 15; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 5.1e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXX 5
 DB 4 FSRDW 8

RESULT 5
 COXA THUOB
 ID COXA THUOB STANDARD; PRT; 20 AA.
 AC P80972;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome c oxidase polypeptide Va-1 (Ec 1.9.3.1) (Fragment).
 OS Thunnus obesus (Bigeye tuna).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorphna; Acanthopterygii; Perciformes; Scombroidei;
 CC Scombridae; Thunnus.
 NCBI_TaxID=8241;
 [1]
 RN RP SEQUENCE.
 RC TISSUE=Heart, and Liver;
 RX MEDLINE=97454291; PubMed=9310366;
 RA Arnold S., Lee T., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver."
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
 CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.

CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferri-cyclochrome c + 2 H(2)O.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
 DR InterPro: IPR003204; Cyt_c-ox5a.
 DR Pfam: PF02284; COX5a; 1.
 KM Oxidoreductase; Heme; Mitochondrion; Inner membrane.
 FT NON_TER 20
 FT MOD_RES 20
 SQ SEQUENCE 20 AA: 2404 MW: 7E82E43B7157355E CRC64;
 Query Match 75.0%; Score 15; DB 1; Length 20;
 Best local Similarity 40.0%; Pred. No. 8.6e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 DB 11 FQARW 15
 RESULT 6
 AKH_TABAT STANDARD; PRT: 8 AA.
 AC P14595.
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor 1)
 OS Tabanus atratus (Horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Tabanomorpha; Tabanidae; Tabanus.
 OX NCBI_TaxID=7207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90046758; PubMed=2813385;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuroepitope hormones with adipokinetic and
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HTH / RPCH FAMILY.
 CC PIR: A33995; A33995.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KM Neuropeptide; Amidation; Flight.
 FT MOD_RES 1
 FT MOD_RES 8
 FT MOD_RES 1
 SQ SEQUENCE 8 AA: 949 MW: 86786771A9D1A736 CRC64;
 Query Match 70.0%; Score 14; DB 1; Length 8;
 Best local Similarity 40.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 DB 4 FPPGW 8
 RESULT 7
 HTF1_PERAM STANDARD; PRT: 8 AA.
 AC P04548;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hypertrehalosemic factor 1 (Neuropeptide M-1) (Periplaneta CC-1)

DE (Pea-CAH-I) (Leb-CC-I) (Hypertrehalosemic neuropeptide I).
 OS Periplaneta americana (American cockroach),
 OS Lepidoptera decemlineata (Colorado potato beetle), and
 OS Blattella orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattellidae; Blattella; Periplaneta.
 OX NCBI_TaxID=6978, 7539, 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Wilten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L., Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry";
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L., Jr.;
 RT "Primary structures of hypertrehalosemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphadorhina portentosa, Blattella germanica and Blattella orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -1- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HTH / RPCH FAMILY.
 CC PIR: A05169; A05169.
 DR PIR: S08995; S08995.
 DR PIR: A49823; A49823.
 DR PIR: A44960; A44960.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KM Neuropeptide; Amidation.
 FT MOD_RES 1
 FT MOD_RES 8
 FT MOD_RES 1
 SQ SEQUENCE 8 AA: 991 MW: 86745775B9C452D6 CRC64;
 Query Match 70.0%; Score 14; DB 1; Length 8;
 Best local Similarity 40.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 DB 4 FSPNW 8
 RESULT 8
 HTF2_PERAM STANDARD; PRT: 8 AA.
 ID HTF2_PERAM

AC P04549; 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hypertrihaloemic factor II (Neuropeptide M-II) (Periplaneta CC-2)
 DE (Pep-CAH-II) (Lep-CC-II) (Hypertrihaloemic neuropeptide II).
 OS Periplaneta americana (American cockroach).
 OS Leptinotarsa decemlineata (Colorado potato beetle), and
 OS Blattella orientalis (Oriental cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blattodea; Blattella; Periplaneta.
 OX NCBI_TaxID=6978, 7539, 6976;
 RX SPECIES=P.americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Wilten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L., Jr.;
 RA "Structures of two cockroach neuropeptides assigned by fast atom
 bombardment mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.
 RP SPECIES=P.americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RA "Isolation and primary structure of two peptides with
 cardiac accelerator and hyperglycemic activity from the corpora
 cardiaca of Periplaneta americana.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RE SEQUENCE.
 RE SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.;
 RA "The metabolic neuropeptides of the corpus cardiaca from the potato
 beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RP SEQUENCE.
 RP SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L., Jr.;
 RA "Primary structures of hypertrihaloemic neuropeptides isolated from
 the corpora cardiaca of the cockroaches Leucophaea maderae,
 Gryllodromia porteri, and the stick insect Exaltosoma titatum assigned by tandem fast
 atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -1- FUNCTION: HYPERTRIHALOEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: A05170; A05170.
 DR PIR: S08996; S08996.
 DR PIR: B44960; B44960.
 DR PIR: B49823; B49823.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD.RES 1 8
 FT MOD.RES 8 8
 SQ SEQUENCE 8 AA; 1006 MW; 86745771ADDA736 CRC64;
 PYRROLIDONE CARBOXYLIC ACID.
 AMIDATION.
 Query Match 70.0%; Score 14; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 9
 HTF_TENMO STANDARD; PRT; 8 AA.
 AC P25419;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hypertrihaloemic factor (HRTN) (Hypertrihaloemic neuropeptide).
 OS Tenebrio molitor (Yellow mealworm), and
 OS Zophobas rugipes.
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 CC Cucujiformia; Tenebrionidae; Tenebrio.
 OX NCBI_TaxID=7067, 7075;
 RX SPECIES=
 RX TISSUE=Corpora cardiaca;
 RX MEDLINE=90341081; PubMed=2381871;
 RA Gaede G., Rosinski G.;
 RA "The primary structure of the hypertrihaloemic neuropeptide from
 tenebrionid beetles: a novel member of the AKH/RPCH family.";
 RL Peptides 11:455-459(1990).
 CC -1- FUNCTION: HYPERTRIHALOEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: A43976; A43976.
 DR PIR: B43976; B43976.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD.RES 1 8
 FT MOD.RES 8 8
 SQ SEQUENCE 8 AA; 1005 MW; 8674575B9C44736 CRC64;
 PYRROLIDONE CARBOXYLIC ACID.
 AMIDATION.
 Query Match 70.0%; Score 14; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 10
 RPCH_PANBO STANDARD; PRT; 8 AA.
 AC P08939;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Red pigment concentrating hormone (RPCH).
 OS Pandanus borealis (Northern red shrimp).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 CC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 CC Caridea; Pandaloidea; Pandallidae; Pandanus.
 OX NCBI_TaxID=6703;
 RN [1]
 RP SEQUENCE.
 RP MEDLINE=75054965; PubMed=4433569;
 RA Fernlund P.;
 RA "Structure of the red-pigment-concentrating hormone of the shrimp,
 Pandanus borealis.";
 RL Biochim. Biophys. Acta 371:304-311(1974).
 CC -1- FUNCTION: THIS HORMONE ADAPTS THE ANIMAL TO LIGHT BACKGROUNDS BY
 CC STIMULATING CONCENTRATION OF THE PIGMENT OF ITS RED BODY-
 CC CHROMATOPHORES.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: S07139; S07139.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.

KW	Pigment; Hormone; Amidation.
FT	MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT	MOD_RES 8 8 AMIDATION
SO	SEQUENCE 8 AA; 948 MM; 86786775B9C44736 CRC64;
Qy	Query Match 70.0%; Score 14; DB 1; Length 8; Best Local Similarity 40.0%; Pred.No. 1.le+05; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy	1 FXXNW 5 1
Db	4 ESPGW 8
RESULT 11	
HTEF_ROMMI	
ID	HTEF_ROMMI STANDARD; PRT; 10 AA.
AC	P18110.
DT	01-NOV-1990 (Rel. 16, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DT	01-FEB-1994 (Rel. 28, Last annotation update)
DE	RO I (Hypertrehalosaemic factor).
OS	Romalea microptera (lubber grasshopper).
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC	Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Celliitera;
OC	Acridomorpha; Acridoidea; Romaleidae; Romalea.
OX	NCBI_TaxID=7007;
RN	[1]
RP	SEQUENCE.
RC	TISSUE=Corpora cardiaca;
RX	MEDLINE=89145002; PubMed=3226948;
RA	Gaele G., Beyreuther K., Rinehart K.L. Jr.:
RT	"Sequence analysis of two neuropeptides of the AKH/Rpch-family from
RT	the lubber grasshopper, Romalea microptera.";
RL	Peptides 9:681-688(1988).
CC	-I- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC	ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH OF INSECTS).
CC	THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC	-I- SIMILARITY: BELONGS TO THE AKH / HRTH / Rpch FAMILY.
DR	InterPro; IPRO02047; AKH.
DR	PROSITE; PS00256; AKH; 1.
KW	Neuropeptide; Amidation; Flight.
FT	MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT	MOD_RES 10 10 AMIDATION.
SQ	SEQUENCE 10 AA; 1163 MM; 056236745771A9C4 CRC64;
Qy	Query Match 70.0%; Score 14; DB 1; Length 10; Best Local Similarity 40.0%; Pred.No. 8.e+02; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy	1 FXXNW 5 1
Db	4 FTPNM 8
RESULT 12	
HTEF_CARMO	
ID	HTEF_CARMO STANDARD; PRT; 10 AA.
AC	P11385.
DT	01-JUL-1989 (Rel. 11, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	Hypertrehalosaemic factor II (HTF-II) (HRTH-II) (Hypertrehalosaemic
DE	neuropeptide II).
OS	Carausius morosus (Indian stick insect), and
OS	Extatosoma tiaratum (Stick Insect).
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC	Insecta; Pterygota; Neoptera; Orthopteroidea; Phasmatodea;
OC	Heteromellidae; Carausius.
OX	NCBI_TaxID=7022, 7024;
RN	[1]
RP	SEQUENCE.
RC	SPECIES=C.morosus; TISSUE=Corpora cardiaca;

RA	MEDLINE=87157103; PubMed=3828078; Rinehart K.L. Jr.;
RA	Gaele G., Rinehart K.L. Jr.;
RT	"Primary structure of the hypertrehalosemic factor II from the
RT	corpus cardiacum of the Indian stick insect, <i>Carausius morosus</i> ,
RT	determined by fast atom bombardment mass spectrometry.";
RL	Biol. Chem. Hoppe-Seyler 368:67-75(1987).
RN	(2)
RP	SEQUENCE.
RC	SPECIES= <i>E. latratum</i> ; TISSUE=Corpora cardiaca;
RX	MEDLINE=90253659; PubMed=2340112; Gaele G., Rinehart K.L. Jr.;
RA	"Primary structures of hypertrehalosemic neuropeptides isolated from
RT	the corpora cardiaca of the cockroaches <i>Leucophaea maderae</i> ,
RT	<i>Gromphadorhina portentosa</i> , <i>Blattella germanica</i> and <i>Blatta orientalis</i>
RT	and of the stick insect <i>Extatosoma latratum</i> assigned by tandem fast
RT	atom bombardment mass spectrometry.";
RL	Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN	(3)
RP	CARBOHYDRATE-LINKAGE SITE.
RC	SPECIES= <i>C. morosus</i> ; TISSUE=Corpora cardiaca;
RX	MEDLINE=93129188; PubMed=1482345; Gaele G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
RA	"A tryptophan-substituted member of the AKH/RPCH family isolated from
RT	a stick insect corpus cardiacum.";
RL	Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
CC	-1- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
CC	ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC	THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC	-1- MASS SPECTROMETRY: MW=1308.61; METHOD=FAb.
CC	-1- SIMILARITY: BELONGS TO THE AKH / RPCH / RPCH FAMILY.
DR	PIR: S07157; S07157.
DR	PIR: S09138; S09138.
DR	InterPro: IPR002047; AKH.
DR	PROSITE: PS00256; AKH; 1.
KW	Neuropeptide; Amidation; Glycoprotein.
FT	MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT	CARBOHYD 8 8 C-LINKED (MAN) (PROBABLE).
FT	MOD_RES 10 10 AMIDATION.
SO	SEQUENCE 10 AA: 1164 MW: 989036745771AD91 CRC64;
OY	1 FXXXX 5 70.0%; Score 14; DB 1; Length 10;
DB	4 FPPNW 8 Best Local Similarity 40.0%; Pred. No. 8.8e+02;
	Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
RESULT 13	
HFE_NAUCI	
ID	STANDARD: PRT: 10 AA.
AC	P10939;
DT	01-JUL-1989 (Rel. 11, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Hypertrehalosemic hormone (HRH) (Hypertrehalosemic neuropeptide).
OS	Nauphoeta cinerea (cinnereus cockroach) (Gray cockroach),
OS	Leucophaea maderae (Madeira cockroach), and
OS	Blattella germanica (German cockroach), and
OS	Gromphadorhina portentosa (Madagascan hissing cockroach).
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC	Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC	Blaberidae; Blaberidae; Nauphoeta.
OX	NCBI_TaxID=6990, 6988, 6973, 36953;
RN	(1)
RP	SEQUENCE.
RC	SPECIES= <i>N. cinerea</i> ; TISSUE=Corpora cardiaca;
RA	MEDLINE=87100208; PubMed=3801028; Gaele G., Rinehart K.L. Jr.;
RT	"Amino acid sequence of a hypertrehalosemic neuropeptide from the
RT	corpus cardiacum of the cockroach, <i>Nauphoeta cinerea</i> .";
RL	Biochem. Biophys. Res. Commun. 141:774-781(1986).

```

RN [2]
RP SEQUENCE.
RC SPECIES=L.maderae, G.portentosa, and B.germanica;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrichosemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Grampodorthina portentosa, Blattella germanica and Blattia orientalis
RT and of the stick insect Exaltosoma flaratum assigned by tandem fast
RT atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN [3]
RP SEQUENCE.
RC SPECIES=B.germanica;
RX MEDLINE=91179584; PubMed=2080017;
RA Veenstra J.A., Camps F.;
RT "Structure of the hypertrichosemic neuropeptide of the German
RT cockroach, Blattella germanica."
RL Neuropeptides 15:107-109(1990).
CC -1- FUNCTION: HYPERTRICHOSEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A26381; A26381.
DR PIR: S08997; S08997.
DR PIR: S08998; S08998.
DR PIR: S09137; S09137.
DR PIR: A60421; A60421.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KM Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA: 1092 MW: 056236786775B9C4 CRC64:

Query Match
Best Local Similarity 70.0%; Score 14; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 4 FSPGW 8

RESULT 14
HT? TABAT
ID HTF TABAT STANDARD: PRT; 10 AA.
AC P14596;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 01-FEB-1994 (Rel. 28, Last annotation update)
DE Hypertrichosemic factor (HOTH) (Dipteran corpora cardiaca factor II)
DE (DCC II).
OS Tabanus atratus (Horse fly).
CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
CC Tabanomorpha; Tabanidae; Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -1- FUNCTION: HYPERTRICHOSEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: B33995; B33995.

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DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KM Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1169 MW: 916036786771A9D1 CRC64:

Query Match
Best Local Similarity 70.0%; Score 14; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 4 FSPGW 8

RESULT 15
YPNP_PHOTO
ID YPNP_PHOTO STANDARD: PRT; 13 AA.
AC P41122;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PNP 3' region (ORF3) (Fragment).
OS Photobacterium luminescens (Xenobacterium luminescens).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Photobacterium.
OX NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K122;
RX MEDLINE=94266731; PubMed=8206856;
RA Clarke D.J., Dowds B.C.A.;
RT "The gene coding for polynucleotide phosphorylase in Photobacterium sp.
RT strain K122 is induced at low temperatures."
RL J. Bacteriol. 176:3775-3784(1994).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X76069; CAA53672.1; -.
KM Hypothetical protein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1634 MW: 64774A4F6267A364 CRC64:

Query Match
Best Local Similarity 70.0%; Score 14; DB 1; Length 13;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 3 FFLRW 7

```

Search completed: January 29, 2003, 14:17:03
 Job time : 10 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

Run on: January 29, 2003, 14:15:28 ; Search time 28 Seconds
(without alignments)
36.794 Million cell updates/sec

```
Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXW 5
```

Scoring table:	BLOSUM62	Gapnext 0 5
	Gapopen 10 0	

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 63395

```
Minimum DB seq length: 0
Maximum DB seq length: 20
```

```
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
```

```

1:  sp.archaea:*
2:  sp.bacteria:*
3:  sp.fungi:*
4:  sp.human:*
5:  sp.invertebrate:*
6:  sp.mammal:*
7:  sp.mhc:*
8:  sp.organelle:*
9:  sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.virussimplied:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	17	85.0	13	8	09XLI12	09XLI12 hemisia tab
2	16	80.0	11	8	09G649	09G649 otiocryptis
3	16	80.0	17	4	015276	015276 homo sapien
4	16	80.0	19	15	091329	091329 human immun
5	16	80.0	9	15	09WJBI1	09WJBI1 human immun
6	15	75.0	9	8	08WCE6	08WCE6 procamburus
7	15	75.0	10	8	09ZYI2	09ZYI2 ieloccephalu
8	15	75.0	10	8	P92707	P92707 platysaurus
9	15	75.0	10	8	079897	079897 hoplocercus
10	15	75.0	11	8	09G368	09G368 diaco bianf
11	15	75.0	11	8	09G646	09G646 sitana pont
12	15	75.0	11	8	09G643	09G643 calotes cal
13	15	75.0	11	8	09G640	09G640 calotes cey
14	15	75.0	11	8	09G634	09G634 calotes lio
15	15	75.0	11	8	09G631	09G631 calotes nig
16	15	75.0	11	8	09G365	09G365 calotes emm

17	15	75.0	11	8	Q9G628	calotes mys
17	15	75.0	11	8	Q9G625	calotes var
18	15	75.0	11	8	Q9G601	branchocela
19	15	75.0	11	8	Q9G522	pseudocalot
20	15	75.0	11	8	Q9G529	pseudocalot
21	15	75.0	11	8	Q9G559	pseudocalot
21	15	75.0	11	8	Q9G559	pseudocalot
22	15	75.0	11	8	Q9G559	pseudocalot
23	15	75.0	20	6	Q9R5E8	baellius sp
24	15	75.0	20	6	Q9R5E8	baellius sp
25	14	70.0	10	8	Q9ZYS6	stenocephalus
26	14	70.0	10	8	Q9ZYS6	stenocephalus
27	14	70.0	10	8	Q9ZYS6	stenocephalus
28	14	70.0	10	8	Q9ZYS6	stenocephalus
29	14	70.0	10	8	Q9ZYS6	stenocephalus
30	14	70.0	10	8	Q9ZYS6	stenocephalus
31	14	70.0	10	8	Q9ZYS6	stenocephalus
32	14	70.0	10	8	Q9ZYS6	stenocephalus
33	14	70.0	10	8	Q9ZYS6	stenocephalus
34	14	70.0	10	8	Q9ZYS6	stenocephalus
35	14	70.0	10	8	Q9ZYS6	stenocephalus
36	14	70.0	10	8	Q9ZYS6	stenocephalus
37	14	70.0	10	8	Q9ZYS6	stenocephalus
38	14	70.0	10	8	Q9ZYS6	stenocephalus
39	14	70.0	10	8	Q9ZYS6	stenocephalus
40	14	70.0	10	8	Q9ZYS6	stenocephalus
41	14	70.0	10	8	Q9ZYS6	stenocephalus
42	14	70.0	10	8	Q9ZYS6	stenocephalus
43	14	70.0	10	8	Q9ZYS6	stenocephalus
44	14	70.0	10	8	Q9ZYS6	stenocephalus
45	14	70.0	12	2	Q53579	rhodobacter

ALIGNMENTS

	RESULT 1				
ID	09XLI2	PRELIMINARY:	PRT:	13 AA.	
AC	09XLI2;				
DT	01-NOV-1999 (TrEMBLrel. 12, Created)				
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)				
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)				
DE	Cytochrome oxidase I (Fragment).				
OS	Bemisia tabaci (Sweetpotato whitefly).				
OG	Mitochondrion.				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;				
CC	Aleyrodiformes; Aleyrodidae; Aleyrodinae; Bemisia.				
OX	NCBI_TaxID=7038;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	PubMed=10583831;				
RA	Frolich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,				
RA	Brown J.K.;				
RT	"A phylogeographical analysis of the Bemisia tabaci species complex based on mitochondrial DNA markers."				
RL	Mol. Ecol. 8:1683-1691(1999).				
KR	EMBL: AF110703; AM28415.1; -.				
KW	Mitochondrion.				
FT	NON TER	1			
SQ	SEQUENCE	13 AA;	1639 MW;	8DD68729F5744365 CRC64;	
	Query Match	85.0%;	Score 17;	DB 8;	Length 13;
	Best Local Similarity	40.0%;	Pred. No. 8.2e+02;		
	Matches	2; Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0
Oy	1 FXXXW 5				
Ds	3 FTSSW 7				
	RESULT 2				
ID	09G649	PRELIMINARY:	PRT:	11 AA.	
	09G649				

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AC 096649;
LT 01-MAR-2001 (TREMBlrel. 16, Created)
LT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
LT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
LE Cytochrome c oxidase subunit I (Fragment).
GN COI.
CS Otolocryptis wlegmanni.
CC Mitochondrion.
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Lepidodonta; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
CC Otolocryptis.
CX NCBI_TaxID=118220;
RN [1]
RP SEQUENCE FROM N.A.
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RL structural features illustrated with acrodont lizards.";
RN [2]
RP SEQUENCE FROM N.A.
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pechiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-ethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL: AF128480; AAC00677.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 11 AA; 1347 MW; 932D3710D3640DC1 CRC64;

Query Match
Best Local Similarity 80.0%; Score 16; DB 8; Length 11;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 3 FTARW 7

RESULT 3
ID 015276 PRELIMINARY; PRT; 17 AA.
AC 015276;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Mitochondrial translation elongation factor EF-Tu (Fragment).
GN TUFW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jacobs H.T., Smurthwaite L., Koshy R.;
RT "Human genome sequences encoding mitochondrial elongation factor EF-
RT Tu: Evidence for post-endosymbiotic Intron Insertion.";
RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: Y11197; CA72493.1; -.
KW Elongation factor.
FT NON_TER
SQ SEQUENCE 17 AA; 2019 MW; BF737D12D2AB0A7E CRC64;

Query Match
Best Local Similarity 80.0%; Score 16; DB 4; Length 17;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 1 FSLTW 5

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RESULT 4
ID 091329 PRELIMINARY; PRT; 19 AA.
AC 091329;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Belc L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,
RA Safar M., Barre-Sinoussi F., Kazatchkine M.D.;
RT "Genetically related human immunodeficiency virus type 1 in three
RT adults of a family with no identified risk factor for intrafamilial
RT transmission.";
RL J. Virol. 72:5831-5839(1998).
DR EMBL: U87220; AAC32980.1; -.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER
SQ SEQUENCE 19 AA; 2324 MW; 379CB14A9E073911 CRC64;

Query Match
Best Local Similarity 80.0%; Score 16; DB 15; Length 19;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 10 FNSTW 14

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RESULT 5
ID 09WJBI PRELIMINARY; PRT; 19 AA.
AC 09WJBI;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Belc L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,
RA Safar M., Barre-Sinoussi F., Kazatchkine M.D.;
RT "Genetically related human immunodeficiency virus type 1 in three
RT adults of a family with no identified risk factor for intrafamilial
RT transmission.";
RL J. Virol. 72:5831-5839(1998).
DR EMBL: U87216; AAC32976.1; -.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER
SQ SEQUENCE 19 AA; 2294 MW; 3781714A9E073911 CRC64;

Query Match
Best Local Similarity 80.0%; Score 16; DB 15; Length 19;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 10 FNSTW 14

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RESULT 6
ID 08WGE6 PRELIMINARY; PRT; 9 AA.
QY 1 FXXXW 5
DB 10 FNSTW 14

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AC Q8WSE6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
OS Procamburus clarkii (Red swamp crayfish).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacidae; Cambaridae; Procambarus.
OX NCBI_TaxID=6728;
RN [1]
RP SEQUENCE FROM N.A.
RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
RA Cunningham C.W.;
RT "Mitochondrial gene rearrangements support a hypothesis of parallel
RT evolution to the crab-like form."
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF436024; AAL31599.1; -.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1185 MW; 936BB9C733640321 CRC64;

Query Match 75.0%; Score 15; DB 8; Length 9;
Best Local Similarity 40.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 1 FTKRW 5

RESULT 7
09ZYT2 PRELIMINARY; PRT; 10 AA.
AC 09ZYT2;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Leiocephalus carinatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae;
OC Leiocephalus.
OX NCBI_TaxID=81825;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99162288; PubMed=10051389;
RA Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT "Molecular tests of phylogenetic taxonomies: A general procedure and
RT example using four subfamilies of the lizard family Iguanidae."
RL Mol. Phylogenet. Evol. 10:367-376(1998).
DR EMBL; AF049864; AAD02535.1; -.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;

Query Match 75.0%; Score 15; DB 8; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 2 FTKRW 6

RESULT 8
P92707 PRELIMINARY; PRT; 10 AA.
AC P92707;

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DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Platyseurus capensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidae;
OC Cordylidae; Platyseurus.
OX NCBI_TaxID=52175;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97153826; PubMed=9000757;
RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
RT "Two novel gene orders and the role of light-strand replication in
RT rearrangement of the vertebrate mitochondrial genome."
RL Mol. Biol. Evol. 14:91-104(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
RT structures of mitochondrial transfer RNAs."
RL Mol. Biol. Evol. 14:30-39(1997).
DR EMBL; U71329; AAB48286.1; -.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1322 MW; 0A3480C9D36415B0 CRC64;

Query Match 75.0%; Score 15; DB 8; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 2 FTKRW 6

RESULT 9
079897 PRELIMINARY; PRT; 10 AA.
AC 079897;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Hoplocercus spinosus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hoplocercinae;
OC Hoplocercus.
OX NCBI_TaxID=52193;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97315309; PubMed=9169559;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Evolutionary shifts in three major structural features of the
RT mitochondrial genome among Iguanian lizards."
RL J. Mol. Evol. 44:660-674(1997).
DR EMBL; U82683; AAC62284.1; -.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 75.0%; Score 15; DB 8; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 2 FTKRW 6

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RESULT 10
Q9G368
ID 09G368 PRELIMINARY: PRT: 11 AA.
AC 09G368:
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DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DI: Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Draco blanfordii.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Draco.
OX NCBI_TaxID=89021;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RL Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
RT structures of mitochondrial transfer RNAs.";
RL Mol. Biol. Evol. 14:30-39(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RX Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Relays migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DF EMBL; AF128477; AAG00668.1; -.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1341 MW; 4B2D371E336415B7 CRC64;

Query Match 75.0%; Score 15; DB 8; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 3 FLSRW 7

RESULT 11
Q9G646
ID 09G646 PRELIMINARY: PRT: 11 AA.
AC 09G646:
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DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Sitana ponticeriana.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Sitana.
OX NCBI_TaxID=118235;
RN [1]
RP SEQUENCE FROM N.A.
RX Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]

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RP SEQUENCE FROM N.A.
RX Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RX Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Relays migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128481; AAG00680.1; -.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1355 MW; 0A2D371E336411A0 CRC64;

Query Match 75.0%; Score 15; DB 8; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 3 FTRRW 7

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AC 09G643:
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DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Calotes calotes.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=118093;
RN [1]
RP SEQUENCE FROM N.A.
RX Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RX Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Relays migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128482; AAG00683.1; -.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1373 MW; BE2D371E336411A6 CRC64;

Query Match 75.0%; Score 15; DB 8; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 3 FTRRW 7

RESULT 13
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AC 09G640:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Calotes ceylonensis.
OC Mitochondrion.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=118094;
RN [1]
RP SEQUENCE FROM N.A.
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL: AF128483; AAG00686.1; -.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA: 1355 MW: 4B2D371E336411A7 CRC64;

Query Match 75.0%; Score 15; DB 8; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
DB 3 FLTRW 7

RESULT 14
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AC O9G634;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Calotes lilolepis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=118096;
RN [1]
RP SEQUENCE FROM N.A.
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL: AF128485; AAG00692.1; -.
KW Mitochondrion.
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SQ SEQUENCE 11 AA: 1355 MW: 4B2D371E336411A7 CRC64;

Query Match 75.0%; Score 15; DB 8; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
DB 3 FLTRW 7

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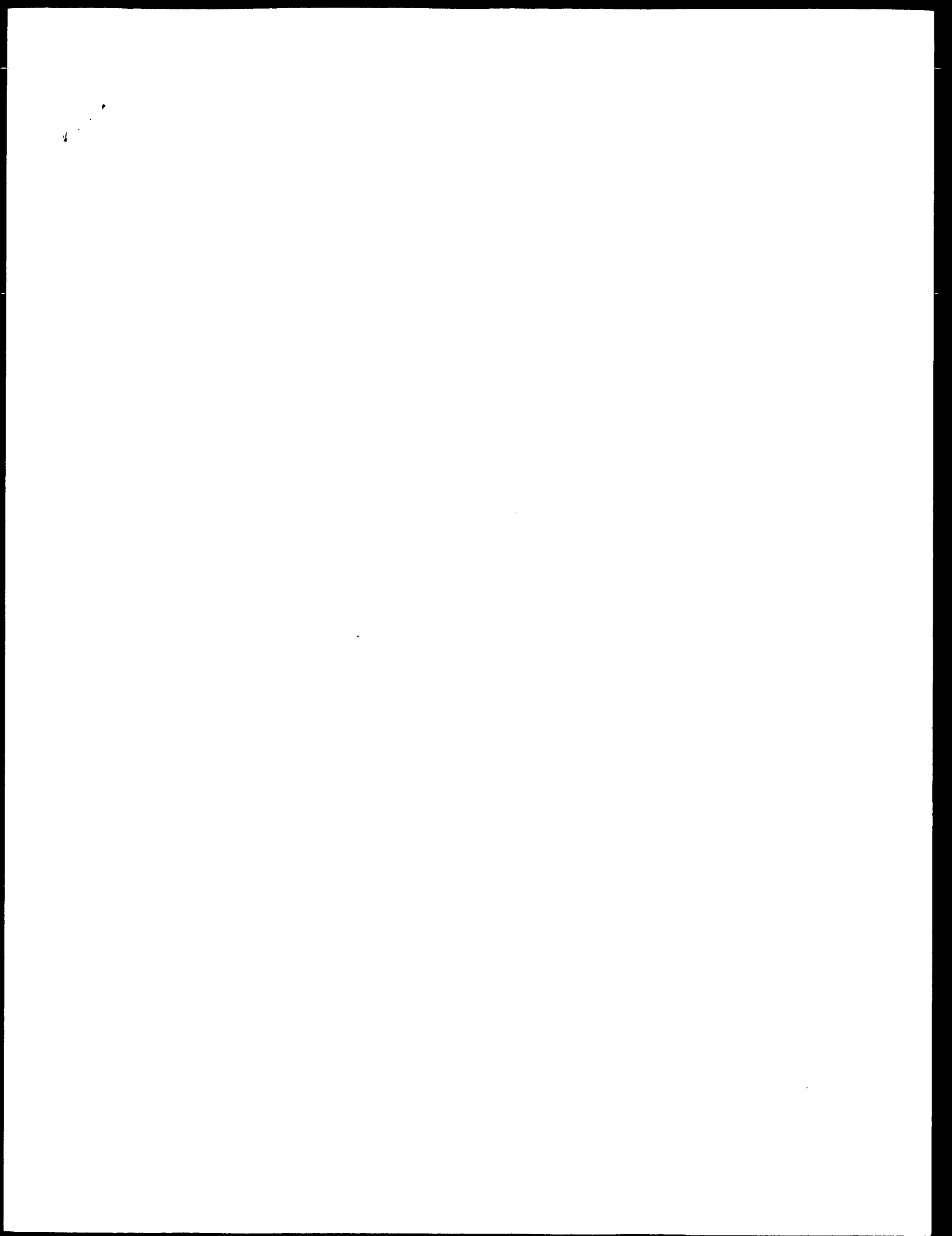
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ID O9G631;
AC O9G631;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Calotes nigrilabris.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=118098;
RN [1]
RP SEQUENCE FROM N.A.
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL: AF128486; AAG00695.1; -.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA: 1355 MW: 4B2D371E336411A7 CRC64;

Query Match 75.0%; Score 15; DB 8; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
DB 3 FLTRW 7

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Search completed: January 29, 2003, 14:17:38
 Job time : 29 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

Run on: January 29, 2003, 14:12:43 ; Search time 34 Seconds
(without alignments)
19.596 Million cell updates/sec

Title:	US-09-403-440A-4
Perfect score:	20
Sequence:	1 FXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 289567

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	17	85.0	10	21	AA810010	H. pylori beta-ure
2	17	85.0	10	22	AA886058	H. pylori beta-ure
3	17	85.0	10	22	AA886090	H. pylori beta-ure
4	17	85.0	13	22	AAE05735	Complementarity-de
5	17	85.0	14	22	AA898088	Human peptide #136
6	17	85.0	15	17	AA897874	Japan cedar pollen
7	17	85.0	15	17	AA897875	Japan cedar pollen
8	17	85.0	15	19	AAW57758	Residues 16-30 of
9	17	85.0	19	23	AAE23038	Human thioredoxin,
10	17	85.0	20	19	AAW42165	T-cell epitope pep

11	17	85.0	20	22	AAG62939	Complementarity d
12	16	80.0	6	19	AAW76953	Fusion immunoglob
13	16	80.0	8	20	AAV18082	Histamine/serotoni
14	16	80.0	9	20	AAV48085	Immunogenic peptid
15	16	80.0	9	22	AAE01057	Human secreted tum
16	80.0	9	23	ABP47522	N. meningitidis LO	
17	16	80.0	10	6	AAV50792	Sequence of new go
18	16	80.0	10	9	AAAP82754	Example of gonadot
19	16	80.0	10	21	AAAB26393	Human CASB618 prot
20	16	80.0	10	21	AAAB26399	Human CASB618 prot
21	16	80.0	10	22	ABBS2240	Human API-186 tryp
22	16	80.0	10	22	ABBS7229	Breast-cancer asso
23	16	80.0	10	22	AAAB35295	Murine PSCA antibo
24	16	80.0	10	23	AAU72831	Anti-MNG2D hybrid
25	16	80.0	11	23	ABP47662	N. meningitidis LO
26	16	80.0	12	18	AAAB32654	Human platelet gly
27	16	80.0	12	19	AAAW71784	Mimotope capable o
28	16	80.0	12	22	AAAB60021	Internalising pept
29	16	80.0	12	22	AAAR70250	Pan DR-binding pep
30	16	80.0	13	16	AAAR70250	Padre (pan-DR bind
31	16	80.0	13	18	AAW22121	Human Factor V pro
32	16	80.0	13	19	AAW64575	Proinflammatory r
33	16	80.0	13	21	AAAB36289	Universal helper T
34	16	80.0	13	21	AAV52558	Pan-DR binding pep
35	16	80.0	13	22	AAAB73644	Pan-DR-binding pep
36	16	80.0	13	22	AAAB99710	PADRE peptide. Sy
37	16	80.0	13	22	AAAB20154	Pan DR epitope pep
38	16	80.0	13	23	AAU80293	Cladosporium herba
39	16	80.0	14	16	AAAR72636	Human peptide #177
40	16	80.0	14	22	AAAM96495	Human peptide #208
41	16	80.0	15	15	AAAS1932	Antigenic polypept
42	16	80.0	15	17	AAAW07992	gp120 peptide 110.
43	16	80.0	15	19	AAAW76978	Fusion immunoglob
44	16	80.0	15	21	AAAB29726	Ganglioside GM1-bi
45	16	80.0	15	21	AAAB29164	Peptide #8. Unide

ALIGNMENTS

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RESULT 1
AAB10010
ID      AAB10010 standard; Protein; 10 AA

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AACB10010;

DT 01-NOV-2000 (first entry)

H. pylori beta-urease-binding antibody heavy chain CDR1 protein #2

Acid-resistant microorganism; detection; faecal; intestine; infection;

KW CDR; beta-urease

05 Unidentified.

PN WO2000026671-

PD 11-MAY-2000.

PF 29-OCT-1999;

PR 29-OCT-1998; 98EP-012051/
08FEB-0120687

XX
XX
CONNOR CONNEX CMBH

XX

PI Ringels A;
xx

DR WPI; 2000-365741/31.
N-PSDB: AAAA0165

XX

100

PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
 PT pylori, comprises reacting a faecal sample with two binding reagents for
 PT antigens that survive intestinal passage
 XX
 ES Claim 26; Page 22; 84pp; German.

CC This invention describes a novel method for the detection of a mammalian
 CC infection by an acid-resistant microorganism (A) by treating a faecal
 CC sample with at least two different monoclonal antibodies (Mab) (or the
 CC fragments or derivatives) or aptamers (collectively (1)) and detecting
 CC formation of a complex (C) between (1) and the corresponding antigen of
 CC (A). The first and second (1) bind to epitopes of different antigens
 CC (A). These epitopes are present, after passage through the intestines,
 CC in at least some mammals, and have either: (i) their native structure;
 CC or (ii) a structure against which an antibody is produced by an animal
 CC infected or immunized with (A), or its extract. Lysate, derived protein
 CC or fragment, or with a synthetic peptide. Practically all mammals display
 CC at least one of the specified epitopes. The method is used to detect
 CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
 CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus,
 CC M. tuberculosis, C. jejuni and C. pylori. (1) may also be used
 CC therapeutically. The method is direct and non-invasive, and provides an
 CC inexpensive and easily standardizable diagnosis, despite possible
 CC degradation of antigens during passage through the intestines. This
 CC sequence represents a fragment of a H. pylori beta-urease-binding
 CC antibody heavy chain complementarity determining region CDR1 which is
 CC used to illustrate the method of the invention.

SO Sequence 10 AA:

Query Match 85.0%; Score 17; DB 21; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.5e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXW 5
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 Db 4 FSTW 8

RESULT 2
 AAB86058
 ID AAB86058 standard; Peptide: 10 AA.

AC AAB86058;
 XX
 DT 17-JUL-2001 (first entry)

DE H. pylori beta-urease derived antibody light chain CDR1 #1.

XX Heavy chain: light chain; catalase; beta-urease; detection; CDR; antigen;
 KW infection; acid-resistant microorganism; faecal; antibody; diagnosis;
 KW antibacterial; complementarity determining region.

XX Unidentified.

OS WO200127613-A2.

PN 19-APR-2001.

PD 12-OCT-2000; 2000WO-EP10058.

PF 12-OCT-1999; 99EP-0120351.

PR 16-MAR-2000; 2000EP-0105592.

PR 31-MAR-2000; 2000EP-0107028.

PR 10-MAY-2000; 2000EP-0110110.

XX (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

PA Reiter C, Cullmann G, Heppner P, Ringels A, Mueller H, Haindl E;
 PI WPI: 2001-282087/29.

DR N-PSDB; AAF88060.
 XX

PT Detecting infections by acid-resistant microorganisms, particularly for
 PT diagnosing Helicobacter pylori, comprises an immunoassay on a faecal
 PT sample
 XX
 ES Claim 23; Page 17; 89pp; German.

CC This invention describes a novel method for detecting, in a mammal,
 CC infection by an acid-resistant microorganism (A) which comprises reacting
 CC a faecal sample with: (i) a receptor (R) such that a complex is formed
 CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part
 CC complex is formed with Ag, and the formation of a complex detected. R are
 CC specific for an Ag which, after passage through the intestines, at least
 CC in some mammals, retains a native (or corresponding) structure against
 CC which the mammal produces antibodies (when immunized or infected with
 CC (A), or its extracts, lysates or derived proteins (or fragments) or
 CC synthetic peptides). The products of the invention have antibacterial
 CC activity. The method is used to diagnose infection by Helicobacter,
 CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
 CC H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the
 CC progress of treatment. Receptors, particularly antibodies, directed
 CC against Ag can be used therapeutically for treatment of infections. The
 CC method requires only one R to provide a reasonably secure diagnosis
 CC (although use of two R improves sensitivity), so is relatively
 CC inexpensive and more easily standardized. Also it is direct,
 CC non-invasive, suitable for automation and may indicate the stage of an
 CC infection. This sequence represents a complementarity determining region
 CC (CDR) from an antibody generated against a Helicobacter pylori antigen
 CC (catalase or beta-urease) which is used to illustrate the method of the
 CC invention.

SO Sequence 10 AA:

Query Match 85.0%; Score 17; DB 22; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.5e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXW 5
 | |
 Db 4 FSTW 8

RESULT 3
 AAB86090
 ID AAB86090 standard; Peptide: 10 AA.

AC AAB86090;
 XX

DT 17-JUL-2001 (first entry)

DE H. pylori beta-urease derived antibody light chain CDR1 #1.

XX Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
 KW acid-resistant microorganism; complementarity determining region;
 KW CDR; faeces; heavy chain; light chain.

XX Unidentified.

OS WO200127612-A2.

PN 19-APR-2001.

PD 12-OCT-2000; 2000WO-EP10057.

PF 12-OCT-1999; 99EP-0120351.

PR 16-MAR-2000; 2000EP-0105592.

PR 31-MAR-2000; 2000EP-0107028.

XX (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

PA Reiter C, Cullmann G, Lakner M, Truse A, Delnert S, Schwartz G;
 PI WPI: 2001-282086/29.

DR
 XX

DR N-PSDB: AAF88117.
 XX
 XX
 PT detecting infections by acid-resistant microorganisms, particularly for
 PT diagnosing *Helicobacter pylori*, comprises immunochromatographic
 PT detection of antigen in feces.
 PS
 XX
 PS Claim 27: Page 27; 90pp; German.
 CC This invention describes a novel method for detecting infection by an
 CC acid-resistant microorganism (A), in a mammal, using infection by an
 CC immunochromatography. The method is used to diagnose infection by an
 CC acid-resistant microorganism (A), in a mammal, such as *Helicobacter*,
 CC *Campylobacter* or *Mycobacterium*, particularly *H. pylori* (most preferred),
 CC *H. hepatica*, *C. jejuni* and *M. tuberculosis*. The method is rapid, simple,
 CC inexpensive and non-invasive, and may indicate the stage of infection.
 CC A test strip used in the method may include a filter to eliminate
 CC particles present in the sample and only a single receptor provides a
 CC reasonably secure diagnosis, with specificity and selectivity improved
 CC by detecting several epitopes (of catalase) or different antigens
 CC (catalase and beta-urease). The method can be automated. This sequence
 CC represents a complementarity determining region (CDR) from an antibody
 CC raised against the *H. pylori* catalase or beta-urease antigen which is
 CC used to illustrate the method of the invention.
 CC
 SQ Sequence 10 AA:
 XX
 XX
 Query Match 85.0%; Score 17; DB 22; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.5e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FXXXW 5
 | |
 Db 4 FSTSW 8
 RESULT 4
 AAE05735
 ID AAE05735 standard; peptide: 13 AA.
 XX
 AC AAE05735;
 XX
 DT 24-SEP-2001 (first entry)
 XX
 DE Complementarity-determining region 3 (CDR3) of Mophabs #7.
 XX
 KW CDR3: complementarity-determining region 3: monoclonal phage antibody;
 KW Mophabs: antigen.
 XX
 OS Synthetic.
 XX
 PN US6265150-B1.
 XX
 PD 24-JUL-2001.
 XX
 PF 26-MAY-1998; 980S-0085072.
 XX
 PR 07-JUN-1995; 950S-0483633.
 PR 18-SEP-1997; 970S-0932892.
 XX
 PA (BECT) BECTON DICKINSON & CO.
 PA (CRUC-) CRUCCELL HOLLAND BV.
 XX
 PI Terstappen LW, Logtenberg T;
 XX
 DR WPI: 2001-463929/50.
 XX
 XX Obtaining a phage particle, useful for obtaining human antibodies
 PT against known and novel surface antigens, by incubating a phage library
 PT with target cells to allow binding of the antibody fragment to the
 PT antigen.
 XX
 PS Example 6: Column 6; 6pp; English.
 XX

CC The invention relates to a method of obtaining a phage particle
 CC which has an antibody fragment directed against an antigen associated
 CC with the surface of target cells in a heterogeneous cell population.
 CC The method involves incubating a library of phage particles with the
 CC target cells to allow binding of the antibody fragment expressed on
 CC the surface of the phage particles to the antigen associated with
 CC the target cells. The method is useful for obtaining human antibodies
 CC against known and novel surface antigens in their native configuration,
 CC CC expressed on phenotypically defined subpopulations of cells.
 CC The present sequence is complementarity-determining region 3 (CDR3)
 CC of monoclonal phage antibodies (Mophabs) used in the exemplification
 CC of the invention.
 CC
 SQ Sequence 13 AA:
 XX
 XX
 Query Match 85.0%; Score 17; DB 22; Length 13;
 Best Local Similarity 40.0%; Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FXXXW 5
 | |
 Db 6 FASSW 10
 RESULT 5
 AAM98088
 ID AAM98088 standard; peptide: 14 AA.
 XX
 AC AAM98088;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human peptide #1363 encoded by a SNP oligonucleotide.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000MO-US35498.
 XX
 PR 28-DEC-1999; 990S-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkels RA, Leach M;
 XX
 DR WPI: 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosis and treating, e.g.
 PT cancer, autoimmune diseases and infections.
 XX
 PS Disclosure: Page 3967; 4143pp; English.
 XX
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC

C2 The oligonucleotides and the peptides encoded by them may be used in the
 C2 prevention, diagnosis and treatment of diseases associated with
 C2 inappropriate expression of the proteins listed above. Disorders that may
 C2 be prevented, diagnosed and/or treated include multifactorial diseases
 C2 with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 C2 arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 C2 and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 C2 brain, breast, colon and kidney, leukaemia), diseases of the nervous
 C2 system and an infection of pathogenic organisms.

SQ Sequence 14 AA:

Query Match 85.0%; Score 17; DB 22; Length 14;
 Best Local Similarity 40.0%; Pred. No. 2e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Q7 1 FXXXW 5

Db 6 FASTW 10

RESULT 6

AA97874 standard; peptide: 15 AA.

AA97874:

16-AUG-1996 (first entry)

Japan cedar pollen mature allergen Cry j II amino acids 16-30.

Allergen; epitope: overlapping peptide: Cry j II; cedar pollen;

Sugi pollinosis; diagnosis; treatment.

Cryptomeria japonica.

JP08047392-A.

20-FEB-1996.

07-NOV-1994; 94JP-0297840.

26-MAY-1994; 94JP-0134868.

05-NOV-1993; 93JP-0276773.

(MEIP) MEIJI MILK PROD CO LTD.

WPI: 1996-166249/17.

Japan cedar pollen allergen Cry j II epitope - comprises at least
 part of specified 460 amino acid protein

Claim 8; Fig 3; 17pp; Japanese.

AA97871-R97960 are overlapping peptides used for the epitope mapping
 of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
 peptides of it are useful in the diagnosis, prevention and treatment
 of Sugi pollinosis, the allergic reaction to Japan cedar pollen.
 Significant regions of the allergen were identified using the
 overlapping peptides of the full epitope derived from a Cry j II
 antigen-specific T cell line. Amino acids 66-80 (AA97884) and 186-200
 (R978908) of the full mature 460 amino acid allergen are the most
 allergenic of the 90 peptides tested.

SQ Sequence 15 AA:

Query Match 85.0%; Score 17; DB 17; Length 15;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Q7 1 FXXXW 5

Db 9 FASTW 13

RESULT 7

AA97875 standard; peptide: 15 AA.

AA97875:

16-AUG-1996 (first entry)

Japan cedar pollen mature allergen Cry j II amino acids 21-35.

Allergen; epitope: overlapping peptide: Cry j II; cedar pollen;

Sugi pollinosis; diagnosis; treatment.

Cryptomeria japonica.

JP08047392-A.

20-FEB-1996.

07-NOV-1994; 94JP-0297840.

26-MAY-1994; 94JP-0134868.

05-NOV-1993; 93JP-0276773.

(MEIP) MEIJI MILK PROD CO LTD.

WPI: 1996-166249/17.

Japan cedar pollen allergen Cry j II epitope - comprises at least
 part of specified 460 amino acid protein

Claim 8; Fig 3; 17pp; Japanese.

AA97871-R97960 are overlapping peptides used for the epitope mapping
 of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
 peptides of it are useful in the diagnosis, prevention and treatment
 of Sugi pollinosis, the allergic reaction to Japan cedar pollen.
 Significant regions of the allergen were identified using the
 overlapping peptides of the full epitope derived from a Cry j II
 antigen-specific T cell line. Amino acids 66-80 (AA97884) and 186-200
 (R978908) of the full mature 460 amino acid allergen are the most
 allergenic of the 90 peptides tested.

SQ Sequence 15 AA:

Query Match 85.0%; Score 17; DB 17; Length 15;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Q7 1 FXXXW 5

Db 4 FASTW 8

RESULT 8

AA57758 standard; peptide: 15 AA.

AA57758:

17-SEP-1998 (first entry)

Residues 16-30 of Cry j 2.

Cry j 2; Japanese cedar pollen antigen; allergy; immunotherapy;

H1A Class II molecule.

Cryptomeria japonica.

WO9820902-A1.

PD 22-MAY-1998.
 XX 12-NOV-1997; 97WO-JP04129.
 PF 13-NOV-1996; 96JP-0302053.
 PR (MEIP) MEIJI MILK PROD CO LTD.
 PA Dairiki K, Kino K, Kume A, Some T;
 PI WPI; 1998-297617/26.
 DR Peptides derived from Japanese cedar pollen antigens are
 XX immunotherapeutic agents - useful for allergy treatment and typing
 PT HLA class II molecules in allergy sufferers
 CC Claim 12: Page 29; 50pp; Japanese.
 XX This sequence represents residues 16-30 of the Cry j 2 protein, and
 CC is a peptide of the invention. The peptides are derived from Japanese
 CC cedar pollen antigens, and are used as immunotherapeutic agents in the
 CC treatment of allergy. The peptides can be used for identification and
 CC typing of the particular HLA class II molecules in an allergy sufferer,
 CC and also for peptide immunotherapy of an allergy. Using these peptides
 CC the immunotherapy can be targeted more specifically to the requirements
 CC of the individual patient, allowing more effective treatment of an
 CC allergy, including those patients for whom treatment with a conventional
 CC immunotherapeutic agent is ineffective.
 SQ Sequence 15 AA:
 Query Match 85.0%; Score 17; DB 19; Length 15;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2: Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXW 5
 DB 9 FSTAW 13
 RESULT 9
 AAE23038
 ID AAE23038 standard; peptide; 19 AA.
 XX
 AC AAE23038;
 XX
 DT 21-AUG-2002 (first entry)
 DE Human thioredoxin, 47916 peptide.
 XX
 KW Human; thioredoxin; 22108; 47916; haematopoietic disorder; leukaemia;
 KW cancer; lung; breast; thyroid; head; neck; prostate; genitourinary tract;
 KW cardiovascular disease; angina pectoris; arteriosclerosis; heart failure;
 KW brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma;
 KW cytosolic; carcinoma; cardiac; neuroprotective; antiinflammatory;
 KW gene therapy; nootropic.
 XX
 OS Homo sapiens.
 XX
 PN WO200226803-A2.
 PD 04-APR-2002.
 XX
 PF 25-SEP-2001; 2001WO-US29967.
 XX
 PR 25-SEP-2000; 2000US-235049P.
 XX
 PS (MILL-) MILLENIUM PHARM INC.
 PA Bandaru R, Kapeller-Libermann R;
 PI WPI; 2002-416475/44.
 DR
 XX

PT New human thioredoxin nucleic acid and polypeptide molecules,
 PT designated 22108 and 47916, useful for diagnosing, preventing or
 PT treating cancer (e.g. carcinoma), cardiovascular diseases (e.g. heart
 PT failure) or brain disorders -
 XX
 PS Disclosure; Page 11; 124pp; English.
 XX
 CC The invention relates to human thioredoxin nucleic acid and polypeptide
 CC molecules, designated 22108 and 47916. The compound that modulates the
 CC activity or expression of 22108 and 47916 nucleic acid is useful for
 CC treating or preventing a disorder characterised by aberrant activity of
 CC 22108 and 47916-expressing cell, specifically for reducing or inhibiting
 CC the aberrant activity of the 22108 and 47916-expressing cancer cell. The
 CC 22108 and 47916 nucleic acid and polypeptide are useful for diagnosing,
 CC preventing or treating cancer in a subject (e.g. leukaemia), or cancers of
 CC metastatic or haematopoietic disorders (e.g. leukemia), or cancers of
 CC the lung, breast, thyroid, head neck, prostate or genito-urinary tract),
 CC cardiovascular diseases (e.g. angina pectoris, arteriosclerosis or heart
 CC failure) or brain disorders (e.g. brain abscess, meningitis, Alzheimer's
 CC diseases). The thioredoxin DNA is also useful in gene therapy. The
 CC present sequence is human thioredoxin, 47916 peptide.
 SQ Sequence 19 AA:
 Query Match 85.0%; Score 17; DB 23; Length 19;
 Best Local Similarity 40.0%; Pred. No. 2.5e+03;
 Matches 2: Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXW 5
 DB 4 FSATW 8
 RESULT 10
 AAM42165
 ID AAM42165 standard; peptide; 20 AA.
 XX
 AC AAM42165;
 XX
 DT 16-JUN-1998 (first entry)
 DE T-cell epitope peptide 45 from Japanese cypress pollen antigen Chao2.
 XX
 DE Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2;
 KW diagnosis; allergy; spring tree pollen disease; pollinosis.
 XX
 OS Chamaecyparis obtusa.
 XX
 OS WO9747648-A1.
 PN 18-DEC-1997.
 PD 12-JUN-1997; 97WO-JP02031.
 XX
 PF 14-JUN-1996; 96JP-0153527.
 XX
 PR (MEIP) MEIJI MILK PROD CO LTD.
 PA Dairiki K, Kino K;
 PI WPI; 1998-052242/05.
 DR T-cell epitope peptide portion of Japanese cypress pollen antigens
 PT Chao1 and Chao2 - used for diagnosis and treatment of spring tree
 PT pollen disease
 XX
 PS Claim 2: Page 36; 71pp; Japanese.
 XX
 CC The present sequence represents a T-cell epitope peptide from Japanese
 CC cypress pollen antigen Chao2. The present invention describes peptides
 CC which correspond to the T-cell epitope sites on Japanese cypress pollen
 CC antigens Chao1 and Chao2. The peptides can be used as a reagent for the
 CC diagnosis of allergy to Japanese cypress pollen, and as an antigen in

CC the treatment and prevention of spring tree pollen disease in which the
 CC pollinosis involves reactivity to Japanese cypress pollen.
 CC Sequence 20 AA:

QY Query Match 85.0%; Score 17; DB 19; Length 20;
 Best Local Similarity 40.0%; Pred. No. 2.6e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DB 1 FXXXW 5
 8 FATTW 12

RESULT 11
 AAG62999
 ID AAG62999 standard; peptide; 20 AA.

AC AAG62999;
 DT 01-OCR-2001 (first entry)

DI Complementarity determining region 3 (CDR3) of VH chain of clone G101.

KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
 KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
 KW transferrin receptor; neurological disease; Alzheimer's disease;
 KW prion disease; AIDS-related dementia; epilepsy; brain injury.

OS Homo sapiens.

PN WO200144300-A2.

XX 21-JUN-2001.

XX 27-NOV-2000; 2000WO-GB04501.

XX 13-DEC-1999; 99US-0170599.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Webster C, Osbourn J, Ward G, Miller K;

XX WPI; 2001-398131/42.

PT Mixture or panel of antibodies for selecting specific binding members
 PT that cross the blood brain barrier, for use in delivering different
 PT molecules and treating neurological diseases

PS Claim 1; Page 76; 109pp; English.

CC AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
 CC of VL and VH chains of antibodies of the invention. The specification
 CC describes a mixture or panel of 5 different specific binding members,
 CC each comprising an antibody VH and/or VL variable domain and capable,
 CC when displayed on the surface of filamentous bacteriophage particles or
 CC in the case of a specific binding member comprising the D5 VH and/or VL
 CC variable domain when bound to human serum amyloid protein, to pass
 CC through a mammalian blood brain barrier (BBB). The panel is useful for
 CC the selection of specific binding members with a desired property such
 CC as ability to cross BBB, ability to bind endothelial cells or other brain
 CC cell antigen, ability to bind areas of inflammation in the brain or BBB
 CC breakdown or ability to bind intracellular adhesion molecules and to bind
 CC transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
 CC and treatment of human or animal body, including neurological diseases,
 CC such as Alzheimer's disease, prion disease, AIDS-related dementia,
 CC epilepsy and traumatic brain injury and any diseases involving
 CC inflammation occurring within the brain or central nervous system.

XX Sequence 20 AA:

QY Query Match 85.0%; Score 17; DB 22; Length 20;
 Best Local Similarity 40.0%; Pred. No. 2.6e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
 4 FSSSW 8

RESULT 12
 AAW76953

ID AAW76953 standard; peptide; 6 AA.

AC AAW76953;

DT 25-JAN-1999 (first entry)

DE Fusion immunoglobulin heavy chain HIV gp120 B cell epitope #93.

KW B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IGH;
 KW human immune deficiency virus; HIV; tolerance; treatment; therapy;
 KW prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;
 KW microbial infection; autoimmune disease; antibody; apoptosis;
 KW antiviral T cell immunity.

OS Mus sp.

OS Homo sapiens.

PN WO9836087-A1.

XX 20-AUG-1998.

XX 13-FEB-1998; 98WO-US02766.

XX 13-FEB-1997; 97US-0040581.

XX (AMNA-) AMERICAN NAT RED CROSS.

XX Scott D, Zambidis E;

XX WPI; 1998-506315/43.

PT New fusion immunoglobulin heavy chain including gp120 epitopes and
 PT related complete antibodies - DNA, vectors and transformed cells,
 PT used to induce tolerance to the epitopes for treatment of human
 PT immune deficiency virus infection

PS Disclosure; Page 40; 154pp; English.

CC This sequence is an epitope used in the construction of a novel fusion
 CC immunoglobulin heavy chain (IGH) protein with a mammalian, especially
 CC human, IGH chain fused in frame at its N-terminus to one or more human
 CC immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or
 CC transfected cells are used to tolerate subjects to gp120 epitopes and to
 CC maintain this tolerance, particularly for treatment of HIV infection,
 CC optionally together with other therapeutic/prophylactic agents such as
 CC vaccines, chemotherapeutic agents and immune response modifiers. Such
 CC proteins can be used against other diseases where an immune response is
 CC deleterious, e.g. microbial infection, tumours or autoimmune disease.
 CC Induction of tolerance suppresses production of antibodies against gp120,
 CC so prevents or inhibits 'bystander' apoptosis of uninfected T cells that
 CC are bound to gp120 protein, maximising induction of protective antiviral
 CC T cell immunity.

XX Sequence 6 AA:

QY Query Match 80.0%; Score 16; DB 19; Length 6;
 Best Local Similarity 40.0%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
 2 FNSRW 6

RESULT 13
AAV18082
ID AAV18082 standard; peptide: 8 AA.
XX
XX
AC AAV18082;
XX
DT 06-AUG-1999 (first entry)
XX
DE Histamine/serotonin cyclic binding peptide.
XX
KW Histamine binding protein; serotonin binding compound; inflammation;
KW gastric acid secretion; allergy; type I hypersensitivity reaction;
KW asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy;
KW drug allergy; abnormal blood pressure; psychological disorder; vaccine;
KW respiratory disease; coronary heart disease; cellular growth regulator;
KW tissue repair; blood-sucking ectoparasite; therapy.
XX
OS Synthetic.
XX
PN W09927104-A1.
XX
PD 03-JUN-1999.
XX
PF 26-NOV-1998; 98WO-GB03530.
XX
PR 26-JUN-1998; 98GB-0013917.
XX
PR 26-NOV-1997; 97GB-0025046.
XX
PA (OXFORD) OXFORD VACS LTD.
XX
PI Nuttall PA, Paesen GC;
XX
DR WPI: 1999-357841/30.
XX
PT Histamine and serotonin binding compounds useful for the treatment
XX of allergies
XX
PS Claim 9; Page 43; 84pp; English.
XX
CC This sequence is an example of a histamine or serotonin binding
CC compound (A), of the invention. The compounds are useful for regulating
CC the action of histamine and serotonin (in e.g. inflammation and gastric
CC acid secretion), the detection, quantification and removal of histamine
CC or serotonin (in animals, plants, cell cultures, food materials, or
CC humans) and in the treatment of various diseases and allergies
CC (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic
CC rhinitis (hay fever), atopic dermatitis, insect bites and food and drug
CC allergies, abnormal blood pressure, migraine, psychological disorders,
CC respiratory disease, and coronary heart disease). Histamine may also be
CC used to regulate cellular growth and tissue repair. The molecules may
CC also be used as components of vaccines directed against blood-sucking
CC ectoparasites.
XX
SQ Sequence 8 AA:
XX
Query Match 80.0%; Score 16; DB 20; Length 8;
Best Local Similarity 40.0%; Pred. No. 7.7e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 FXXXXW 5
DB 4 FAEAW 8

RESULT 14
AAV48085
ID AAV48085 standard; peptide: 9 AA.
XX
XX
AC AAV48085;
XX
DT 01-DEC-1999 (first entry)
XX
DE Immunogenic peptide having a human leukocyte antigen binding motif #2696.

XX
KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN W09945954-A1.
XX
PD 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US05039.
XX
PR 13-MAR-1998; 98WO-US05039.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX
DR WPI: 1999-551214/46.
XX
PT New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases
XX
PS Claim 1; Page 136; 150pp; English.
XX
CC AAV45390 to AAV48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also
CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
CC response against the antigen from which the peptide is derived.
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
CC normally induced by an antigen in the form of a peptide fragment bound
CC to a HLA molecule, rather than the intact foreign antigen itself, and
CC are particularly important in tumour rejection and in fighting viral
CC infections. The peptides are therefore useful therapeutically to treat
CC or prevent viral infections and cancers in mammals (especially humans)
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
CC They can be administered as vaccines to elicit an immune response in
CC individuals susceptible or otherwise at risk of viral infection or
CC cancer, or used to treat chronic or acute conditions. They are also
CC useful diagnostically, and can be used to induce a cytotoxic T cell
CC response, by contacting a cytotoxic T cell with the peptide e.g. to
CC produce CTLs ex vivo for infusion back into a patient. The
CC polynucleotides encoding the immunogenic peptides are also useful
CC therapeutically and for immunisation as above.
XX
SQ Sequence 9 AA:
XX
Query Match 80.0%; Score 16; DB 20; Length 9;
Best Local Similarity 40.0%; Pred. No. 7.7e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 FXXXXW 5
DB 5 FFSSW 9

RESULT 15
AAE01057
ID AAE01057 standard; peptide: 9 AA.
XX
XX
AC AAE01057;
XX
DT 17-JUL-2001 (first entry)
XX
DE Human secreted tumour antigen 36P6D5 peptide #10.
XX
KW Human; 36P6D5 protein; secreted tumour antigen; therapy; cancer; kidney;

KW bladder; ovary; breast; pancreas; colon; lung; vaccine; cytostatic;
 KW MHC; major histocompatibility complex; human leucocyte antigen; HLA-A2.
 OS Homo sapiens.

PN WO200131015-A2.

PD 03-MAY-2001.

PF 30-OCT-2000; 2000WO-US29894.

PR 28-OCT-1999; 99US-0162417.

XX (UROG-) UROGENESTS INC.

PI Raitano AB, Jakobovits A, Faris M, Afar DEH, Hubert RS;
 PI Mitchell SC;

DR WPI: 2001-308646/32.

PT Detecting presence of cancer expressing 36p6d5 protein in individual by
 PT comparing protein level in test sample to normal sample, where elevated
 PT level of protein in test sample indicates presence of cancer -

PS Claim 18; Page 91; 113pp; English.

CC The present invention relates to a gene and its encoded secreted tumour
 CC antigen, termed 36p6d5. These sequences are used for the diagnosis and
 CC treatment of various cancers which express 36p6d5, such as cancers of
 CC the kidney, bladder, ovary, breast, pancreas, colon and lungs. In normal
 CC individuals 36p6d5 protein, is predominantly expressed in pancreas. With
 CC lower levels of expression in prostate and small intestine. Vaccines
 CC comprising immunogenic protein of 36p6d5 is useful for inhibiting the
 CC development of prostate or colon cancer. Pharmaceutical composition
 CC comprising 36p6d5 protein is useful for diagnosis and/or prognosis of
 CC prostate cancer and other cancers, for modulating or inhibiting the
 CC expression of 36p6d5 genes and/or translation of the 36p6d5 transcripts,
 CC and as therapeutic agents. The present sequence is human 36p6d5 peptide.
 CC This sequence binds to the human MHC (major histocompatibility complex)
 CC class I molecule (human leucocyte antigen) HLA-A2 and its half time of
 CC dissociation is 9.7

XX SQ Sequence 9 AA;

Query Match 80.0%; Score 16; DB 22; Length 9;

Best Local Similarity 40.0%; Pred. NO. 7.7e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5

DB 4 FRSSW 8

Search completed: January 29, 2003, 14:16:46
 Job time : 35 secs

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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:17:43 : Search time 11 Seconds
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9.172 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 122226 seqs, 20178551 residues
Total number of hits satisfying chosen parameters: 36068

Minimum DB seq length: 0
Maximum DB seq length: 20

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Listing first 45 summaries

Database : Published Applications_AA:*
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8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	80.0	7	US-10-046-922-48	Sequence 48, Appl
2	16	80.0	7	US-09-774-639-284	Sequence 284, App
3	16	80.0	9	US-10-046-922-59	Sequence 59, Appl
4	16	80.0	10	US-09-826-290-453	Sequence 453, App
5	16	80.0	13	US-09-949-375A-18	Sequence 18, Appl
6	16	80.0	13	US-09-785-215-19	Sequence 19, Appl
7	16	80.0	13	US-09-894-018-69	Sequence 69, Appl
8	16	80.0	15	US-09-205-658-284	Sequence 284, App
9	16	80.0	18	US-09-205-658-283	Sequence 283, App
10	16	80.0	18	US-09-205-658-285	Sequence 285, App
11	16	80.0	19	US-09-864-761-415A6	Sequence 415A6, A
12	16	80.0	20	US-09-812-528-19	Sequence 19, Appl
13	16	80.0	20	US-09-884-441-411	Sequence 411, App
14	16	80.0	20	US-09-884-441-412	Sequence 412, App
15	16	80.0	6	US-09-486-734A-34	Sequence 34, Appl
16	15	75.0	6	US-09-214-371-83	Sequence 83, Appl
17	15	75.0	6	US-09-732-384-4	Sequence 4, Appl
18	15	75.0	6	US-09-732-384-5	Sequence 5, Appl
19	15	75.0	6	US-10-155-059-1	Sequence 1, Appl

20	15	75.0	7	US-09-912-414-28	Sequence 28, Appl
21	15	75.0	7	US-09-096-749A-36	Sequence 36, Appl
22	15	75.0	8	US-08-424-550B-252	Sequence 252, App
23	15	75.0	8	US-09-214-371-12	Sequence 12, Appl
24	15	75.0	8	US-09-214-371-13	Sequence 13, Appl
25	15	75.0	8	US-09-214-371-21	Sequence 21, Appl
26	15	75.0	8	US-09-214-371-22	Sequence 22, Appl
27	15	75.0	8	US-09-214-371-46	Sequence 46, Appl
28	15	75.0	8	US-09-214-371-47	Sequence 47, Appl
29	15	75.0	8	US-09-214-371-48	Sequence 48, Appl
30	15	75.0	8	US-09-214-371-49	Sequence 49, Appl
31	15	75.0	8	US-09-214-371-52	Sequence 52, Appl
32	15	75.0	8	US-09-908-322-83	Sequence 83, Appl
33	15	75.0	9	US-08-821-739A-49	Sequence 49, Appl
34	15	75.0	9	US-08-821-739A-53	Sequence 53, Appl
35	15	75.0	9	US-09-771-415-16	Sequence 16, Appl
36	15	75.0	9	US-09-771-415-16	Sequence 16, Appl
37	15	75.0	9	US-09-214-371-37	Sequence 37, Appl
38	15	75.0	9	US-09-214-371-38	Sequence 38, Appl
39	15	75.0	9	US-09-764-304-12	Sequence 12, Appl
40	15	75.0	9	US-09-862-260A-13	Sequence 13, Appl
41	15	75.0	9	US-09-780-053-130	Sequence 130, App
42	15	75.0	10	US-09-826-290-390	Sequence 390, App
43	15	75.0	10	US-09-214-371-35	Sequence 35, Appl
44	15	75.0	10	US-09-214-371-36	Sequence 36, Appl
45	15	75.0	10	US-09-767-460-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-10-046-922-48
Sequence 48, Application US/10046922
Patent No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Koivunen, Erkki
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.0
SEQ ID NO 48
LENGTH: 7
TYPE: PRT
ORGANISM: peptide
US-10-046-922-48

Query Match 80.0%; Score 16; DB 9; Length 7;
Best Local Similarity 40.0%; Pred. No. 9.9e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0;
Gaps 0;

QY 1 FXXXW 5
DB 3 FEAAW 7

RESULT 2
US-09-774-639-284
Sequence 284, Application US/09774639
Publication No. US20030003555A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P1
CURRENT APPLICATION NUMBER: US/09/774,639
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 371

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 284
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-774-639-284

Query Match
Best Local Similarity 40.0%; Score 16; DB 9; Length 7;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
|
|
Db 2 FGTSW 6

RESULT 3
US-10-046-922-59
Sequence 59, Application US/10046922
Patent No. US2002016467A1
GENERAL INFORMATION:
APPLICANT: Allitalo, Karl
APPLICANT: Koivunen, Erkki
TITLE OF INVENTION: Kado, Hajime
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046, 922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.0
SEQ ID NO 59
LENGTH: 9
TYPE: PRT
ORGANISM: Peptide
US-10-046-922-59

Query Match
Best Local Similarity 80.0%; Score 16; DB 9; Length 9;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
|
|
Db 4 FEAAW 8

RESULT 4
US-09-826-290-453
Sequence 453, Application US/09826290
Patent No. US2002016468A1
GENERAL INFORMATION:
APPLICANT: Durham, L. Kathryn
APPLICANT: Friedman, David L.
APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
APPLICANT: Kimmel, Lida H.
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Potter, David M.
APPLICANT: Rohlff, Christian
APPLICANT: Silber, B. Michael
APPLICANT: Stieger, Thomas R.
APPLICANT: Sunderland, P. Trey
APPLICANT: Townsend, Robert Reid
APPLICANT: White, Frost
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
FILE REFERENCE: 2572-1-001 N2
CURRENT APPLICATION NUMBER: US/09/826, 290
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US 60/194, 504
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: US 60/253, 647
PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 492
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 453
LENGTH: 10
TYPE: PRT
ORGANISM: homo sapien
US-09-826-290-453

Query Match
Best Local Similarity 80.0%; Score 16; DB 9; Length 10;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
|
|
Db 1 FSGTW 5

RESULT 5
US-09-949-375A-18
Sequence 18, Application US/09949375A
Patent No. US20020172673A1
GENERAL INFORMATION:
APPLICANT: Klysner, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949, 375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic amino acid sequence of SEQ ID NO: 17.
US-09-949-375A-18

Query Match
Best Local Similarity 80.0%; Score 16; DB 9; Length 13;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
|
|
Db 3 FVAAM 7

RESULT 6
US-09-785-215-19
Sequence 19, Application US/09785215
Publication No. US20020187157A1
GENERAL INFORMATION:
APPLICANT: JENSEN, Martin Roland et al.
TITLE OF INVENTION: NOVEL METHOD FOR DOWN-REGULATION OF AMYLOID
FILE REFERENCE: 3631-0107P
CURRENT APPLICATION NUMBER: US/09/785, 215
CURRENT FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial T-cell epitope capable of binding to a large portio
OTHER INFORMATION: of MHC Class II molecules in a variety of animals
US-09-785-215-19

Query Match
Best Local Similarity 80.0%; Score 16; DB 9; Length 13;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
|
|

Db 3 FVAAM 7

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RESULT 7
US-09-894-018-69
; Sequence 69, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Dennis
; APPLICANT: Newman, David
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-2003.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: PADRE sequence
US-09-894-018-69
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Query Match 80.0%; Score 16; DB 10; Length 13;
Best Local Similarity 40.0%; Pred. No. 5.9e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
Db 3 FVAAM 7

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RESULT 8
US-09-205-658-284
; Sequence 284, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-284
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Query Match 80.0%; Score 16; DB 10; Length 15;
Best Local Similarity 40.0%; Pred. No. 6.5e+02;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
Db 9 FSTRW 13

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RESULT 9
US-09-205-658-283
; Sequence 283, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-283
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Query Match 80.0%; Score 16; DB 10; Length 18;
Best Local Similarity 40.0%; Pred. No. 7.3e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
Db 12 FSTRW 16

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RESULT 10
US-09-205-658-285
; Sequence 285, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 285
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-285
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Query Match 80.0%; Score 16; DB 10; Length 18;
Best Local Similarity 40.0%; Pred. No. 7.3e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5

Db 12 FSTRW 16

RESULT 11

US-09-864-761-41546

; Sequence 41546, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: Aecmca-x-1

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US/09/864,761

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263,6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 41546

; LENGTH: 19

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO A1139352.8

; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.9

; US-09-864-761-41546

; Query Match

; 80.0%; Score 16; DB 10; Length 19;

Best Local Similarity 40.0%; Pred. No. 7.6e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXW 5
Db 15 FSHW 19

RESULT 12

US-09-812-528-19

; Sequence 19, Application US/09812528

; Patent No. US20010018210A1

; GENERAL INFORMATION:

; APPLICANT: Bachovchin, William

; APPLICANT: Wallner, Barbara

; TITLE OF INVENTION: STIMULATION OF HEMATOPOIETIC CELLS IN

; FILE REFERENCE: 10248/7015

; CURRENT FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: US 60/060,306

; PRIOR FILING DATE: 1997-09-29

; PRIOR APPLICATION NUMBER: US 09/162,934

; PRIOR FILING DATE: 1998-09-29

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 19

; TYPE: PRT

; ORGANISM: homo sapiens

; US-09-812-528-19

; Query Match

; 80.0%; Score 16; DB 10; Length 20;

; Best Local Similarity 40.0%; Pred. No. 7.8e+02;

; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5

Db 3 FASW 7

RESULT 13

US-09-884-441-411

; Sequence 411, Application US/09884441

; Patent No. US20020119158A1

; GENERAL INFORMATION:

; APPLICANT: Algate, Paul A.

; APPLICANT: Carter, Darrick

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.462C7

; CURRENT FILING DATE: 2001-06-18

; NUMBER OF SEQ ID NOS: 489

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 411

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-884-441-411

; Query Match

; 80.0%; Score 16; DB 10; Length 20;

; Best Local Similarity 40.0%; Pred. No. 7.8e+02;

; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5

Db 11 FASW 15

RESULT 14

US-09-884-441-412

; Sequence 412, Application US/09884441

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; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 412
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-441-412

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Query Match      80.0%; Score 16; DB 10; Length 20;
Best Local Similarity 40.0%; Pred. No. 7.8e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 FXXXW 5
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DB 4 FAISW 8

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RESULT 15
US-09-486-734A-34
; Sequence 34, Application US/09486734A
; Patent No. US20020164732A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Marie-Christine
; APPLICANT: Clier, Florence
; APPLICANT: Erlich, S. Dusko
; APPLICANT: Gautier, Michel
; APPLICANT: Schouler, Catherine
; APPLICANT: Institut National de la Recherche Agronomique
; TITLE OF INVENTION: Resistance Mechanisms to Ic Type R/W
; FILE REFERENCE: 33339/196048
; CURRENT APPLICATION NUMBER: US/09/486,734A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/FR98/01873
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: FR 97/10885
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hsds subunit
US-09-486-734A-34

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Query Match      75.0%; Score 15; DB 9; Length 6;
Best Local Similarity 40.0%; Pred. No. 9.9e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 FXXXW 5
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DB 1 FADPW 5

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Search completed: January 29, 2003, 14:21:23
 Job time : 12 secs

2

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:16:53 : Search time 134 Seconds
(Without alignments)
24.057 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20
Sequence: 1 FXXW 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 694069

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%

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- 10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
- 13: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*
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- 15: /cgn2_6/ptodata/1/paa/US091_COMB.pep.*
- 16: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*
- 17: /cgn2_6/ptodata/1/paa/US093_COMB.pep.*
- 18: /cgn2_6/ptodata/1/paa/US094_COMB.pep.*
- 19: /cgn2_6/ptodata/1/paa/US095_COMB.pep.*
- 20: /cgn2_6/ptodata/1/paa/US096_COMB.pep.*
- 21: /cgn2_6/ptodata/1/paa/US097_COMB.pep.*
- 22: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
- 23: /cgn2_6/ptodata/1/paa/US099_COMB.pep.*
- 24: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
- 25: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
- 27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	17	85.0	9	24	US-10-072-419-3
2	17	85.0	9	24	US-10-072-419-8
3	17	85.0	10	22	US-09-842-776A-28
4	17	85.0	10	24	US-10-089-452-36
5	17	85.0	10	25	US-10-110-410-36
6	17	85.0	11	24	US-10-072-419-37

7	17	85.0	14	17	US-09-355-397C-36	Sequence 36, Appl
8	17	85.0	15	17	US-09-308-027-12	Sequence 12, Appl
9	17	85.0	15	17	US-09-308-027-88	Sequence 88, Appl
10	17	85.0	15	17	US-09-308-027A-12	Sequence 12, Appl
11	17	85.0	15	17	US-09-308-027A-88	Sequence 88, Appl
12	17	85.0	19	23	US-09-963-339-10	Sequence 10, Appl
13	17	85.0	19	25	US-10-145-586-59	Sequence 59, Appl
14	17	85.0	20	16	US-09-202-464-45	Sequence 45, Appl
15	17	85.0	20	16	US-09-240-203B-265	Sequence 265, App
16	17	85.0	20	16	US-09-240-2030-265	Sequence 265, App
17	16	80.0	6	1	PCT-US98-02766-155	Sequence 155, App
18	16	80.0	6	14	US-09-023-934-155	Sequence 155, App
19	16	80.0	7	16	US-09-244-112-284	Sequence 284, App
20	16	80.0	7	21	US-09-774-639-284	Sequence 284, App
21	20	80.0	7	23	US-09-969-730-267	Sequence 267, App
22	22	80.0	7	24	US-10-046-922-48	Sequence 48, Appl
23	23	80.0	8	1	PCT-US02-15590-53	Sequence 51, Appl
24	24	80.0	8	1	PCT-US02-15590-53	Sequence 53, Appl
25	25	80.0	8	1	PCT-US02-15590-198	Sequence 198, App
26	26	80.0	8	1	PCT-US02-15590-200	Sequence 200, App
27	27	80.0	8	1	PCT-US02-15590-202	Sequence 202, App
28	28	80.0	8	1	PCT-US02-15590-204	Sequence 204, App
29	29	80.0	8	1	PCT-US02-15590-206	Sequence 206, App
30	30	80.0	8	1	PCT-US02-15590-225	Sequence 225, App
31	31	80.0	8	1	PCT-US02-15590-227	Sequence 227, App
32	32	80.0	8	1	PCT-US02-15590-229	Sequence 229, App
33	33	80.0	8	1	PCT-US02-15590-231	Sequence 231, App
34	34	80.0	8	1	PCT-US02-15590-233	Sequence 233, App
35	35	80.0	8	1	PCT-US02-15590-235	Sequence 235, App
36	36	80.0	8	1	PCT-US02-15590-237	Sequence 237, App
37	37	80.0	8	1	PCT-US02-15590-239	Sequence 239, App
38	38	80.0	8	19	US-08-555-296B-31	Sequence 31, Appl
39	39	80.0	8	24	US-10-072-419-4	Sequence 4, Appl
40	40	80.0	8	24	US-10-072-419-11	Sequence 11, Appl
41	41	80.0	8	24	US-10-072-419-15	Sequence 15, Appl
42	42	80.0	8	24	US-10-072-419-24	Sequence 24, Appl
43	43	80.0	8	24	US-10-072-419-25	Sequence 25, Appl
44	44	80.0	8	24	US-10-072-419-25	Sequence 25, Appl
45	45	80.0	8	24	US-10-072-419-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-10-072-419-3
: Sequence 3, Application US/10072419
: GENERAL INFORMATION:
: APPLICANT: Schacter, Bernice
: TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in H
: FILE REFERENCE: 10739-1
: CURRENT APPLICATION NUMBER: US/10/072,419
: CURRENT FILING DATE: 2002-02-07
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 3
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Apis mellifera
US-10-072-419-3

Query Match 85.0%: Score 17: DB 24: Length 9:
Best Local Similarity 40.0%: Pred. No. 4.2e+06:
Matches 2: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

QY 1 FXXW 5
DB 4 FTSSW 8
RESULT 2
US-10-072-419-8

```
; Sequence 8, Application US/10072419
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
; US-10-072-419-8
```

```
Query Match
Best Local Similarity 85.0%; Score 17; DB 24; Length 9;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 FXXXW 5
| |
Dt- 4 FTSSW 8
```

```
RESULT 3
; Sequence 28, Application US/09842776A
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarily determining region (CDR1) of an
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease
; OTHER INFORMATION: epitope (alternative sequence)
; US-09-842-776A-28
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```
Query Match
Best Local Similarity 85.0%; Score 17; DB 22; Length 10;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 FXXXW 5
| |
Db 4 FTSSW 8
```

```
RESULT 4
; Sequence 36, Application US/10089452
; GENERAL INFORMATION:
; APPLICANT: Connex Gesellschaft zur Optimierung von Forschung und Entwicklung mbH
; TITLE OF INVENTION: Improved Method for Detecting Acid Resistant Microorganisms in H
; FILE REFERENCE: D 2394 PCT
; CURRENT APPLICATION NUMBER: US/10/089,452
; CURRENT FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: PRT
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```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR
; US-10-089-452-36
```

```
Query Match
Best Local Similarity 85.0%; Score 17; DB 24; Length 10;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 FXXXW 5
| |
Db 4 FTSSW 8
```

```
RESULT 5
; Sequence 36, Application US/10110410
; GENERAL INFORMATION:
; APPLICANT: Connex Gesellschaft zur Optimierung von Forschung und Entwicklung mbH
; TITLE OF INVENTION: Immunochromatographic Rapid Test for Detecting Acid Resistant
; FILE REFERENCE: D 1805 PCT
; CURRENT APPLICATION NUMBER: US/10/110,410
; CURRENT FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR
; US-10-110-410-36
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```
Query Match
Best Local Similarity 85.0%; Score 17; DB 25; Length 10;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 FXXXW 5
| |
Db 4 FTSSW 8
```

```
RESULT 6
; Sequence 37, Application US/10072419
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in H
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vanessa cardui
; US-10-072-419-37
```

```
Query Match
Best Local Similarity 85.0%; Score 17; DB 24; Length 11;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 FXXXW 5
| |
Db 4 FTSSW 8
```

```
RESULT 7
; Sequence 36, Application US/09355397C
```

```

; GENERAL INFORMATION:
; APPLICANT: Sphyron, Giannini
; TITLE OF INVENTION: Mammalian Thiodoxin
; FILE REFERENCE: 102043-100
; CURRENT APPLICATION NUMBER: US/09/355,397C
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/GB98/00263
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: GB 9701710.7
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 14
; TYPE: PRT
; ORGANISM: mammal
; US-09-355-397C-36

```

```

Query Match      85.0%; Score 17; DB 17; Length 14;
Best Local Similarity 40.0%; Pred. No. 2.e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 FXXXW 5
DB 5 FSATW 9

```

```

RESULT 8
; US-09-308-027-12
; Sequence 12, Application US/09308027
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Kino, Koshuke
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
; FILE REFERENCE: 06501/031001
; CURRENT APPLICATION NUMBER: US/09/308,027
; PRIOR FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: PCT/JP97/04129
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: JP 8/302053
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria
; US-09-308-027-12

```

```

Query Match      85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 FXXXW 5
DB 9 FSTAW 13

```

```

RESULT 9
; US-09-308-027-88
; Sequence 88, Application US/09308027
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Kino, Koshuke
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
; FILE REFERENCE: 06501/031001
; CURRENT APPLICATION NUMBER: US/09/308,027
; PRIOR FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: PCT/JP97/04129

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```

; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: JP 8/302053
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria
; US-09-308-027-88

```

```

Query Match      85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 FXXXW 5
DB 4 FSTAW 8

```

```

RESULT 10
; US-09-308-027A-12
; Sequence 12, Application US/09308027A
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Kino, Koshuke
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
; FILE REFERENCE: 06501/031001
; CURRENT APPLICATION NUMBER: US/09/308,027A
; PRIOR FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: PCT/JP97/04129
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: JP 8/302053
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria
; US-09-308-027A-12

```

```

Query Match      85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 FXXXW 5
DB 9 FSTAW 13

```

```

RESULT 11
; US-09-308-027A-88
; Sequence 88, Application US/09308027A
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Kino, Koshuke
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
; FILE REFERENCE: 06501/031001
; CURRENT APPLICATION NUMBER: US/09/308,027A
; PRIOR FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: PCT/JP97/04129
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: JP 8/302053
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 15

```

;; TYPE: PRT
;; ORGANISM: Cryptomeria
US-09-308-027A-88

Query Match 85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 4 FSATW 8

RESULT 12
US-09-963-339-10
; Sequence 10, Application US/09963339
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN
; FILE REFERENCE: 10448-090001
; CURRENT APPLICATION NUMBER: US/09/963,339
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/235,049
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-963-339-10

Query Match 85.0%; Score 17; DB 23; Length 19;
Best Local Similarity 40.0%; Pred. No. 2.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 4 FSATW 8

RESULT 13
US-10-145-586-59
; Sequence 59, Application US/10145586
; GENERAL INFORMATION:
; APPLICANT: Alexandra Glucksmann, Maria
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: M. Galvin, Katherine
; APPLICANT: Welch, Nadine
; APPLICANT: Curtis, Roy A.J.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Kapeller-Liebermann, Rosana
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
; TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LECTINE-RICH
; FILE REFERENCE: 10448-188001
; CURRENT APPLICATION NUMBER: US/10/145,586
; PRIOR FILING DATE: 2002-05-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-586-59

Query Match 85.0%; Score 17; DB 25; Length 19;
Best Local Similarity 40.0%; Pred. No. 2.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5

DB 4 FSATW 8

RESULT 14
US-09-202-464-45
; Sequence 45, Application US/09202464
; GENERAL INFORMATION:
; APPLICANT: Kino, Kohsuke
; APPLICANT: Dairiki, Kazuo
; TITLE OF INVENTION: T-CELL EPITOPE PEPTIDES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/202,464
; FILING DATE: 14-Dec-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO JP97/02031
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: JP 8/153527
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06501-024001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-09-202-464-45

Query Match 85.0%; Score 17; DB 16; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.5e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 8 FATW 12

RESULT 15
US-09-240-203B-265
; Sequence 265, Application US/09240203B
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.;
; APPLICANT: Pollack, Joanne;
; Bond, Julian F.;
; Garman, Richard D.;
; Kuo, Mel-Chang;
; Powers, Steven P.;
; Exley, Mark A.;
; Chen, Xian;
; Shaked, Ze'ev
; TITLE OF INVENTION: Allergenic Proteins And Peptides From
; Japanese Cedar Pollen
; NUMBER OF SEQUENCES: 265

* CORRESPONDENCE ADDRESS:
ADDRESS: Lahive & Cockfield, LLP
STREET: 28 State St
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,203B
FILING DATE: 22-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras, Esq.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-240-203B-265

Query Match 85.0%; Score 17; DB 16; Length 20;
Best Local Similarity 40.0%; Pred No 2.5e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
|
|
Db 12 FSTAW 16

Search completed: January 29, 2003, 14:20:41
Job time : 135 secs

100

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:17:08 ; Search time 18 Seconds
(without alignments)
21.950 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 396018 seqs, 79020188 residues

Total number of hits satisfying chosen parameters: 139460

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2.6/ptodata/2/paa/PC7_NEM_COMB.pep:*
2: /cgn2.6/ptodata/2/paa/US06_NEM_COMB.pep:*
3: /cgn2.6/ptodata/2/paa/US07_NEM_COMB.pep:*
4: /cgn2.6/ptodata/2/paa/US08_NEM_COMB.pep:*
5: /cgn2.6/ptodata/2/paa/US09_NEM_COMB.pep:*
6: /cgn2.6/ptodata/2/paa/US10_NEM_COMB.pep:*
7: /cgn2.6/ptodata/2/paa/US50_NEM_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	80.0	8	US-09-641-528-44	Sequence 44, Appl
2	16	80.0	8	US-09-641-528-734	Sequence 734, Appl
3	16	80.0	8	US-09-641-528-1054	Sequence 1054, Appl
4	16	80.0	8	US-09-641-528-20273	Sequence 20273, A
5	16	80.0	8	US-09-641-528-20303	Sequence 21722, A
6	16	80.0	8	US-09-641-528-21722	Sequence 21757, A
7	16	80.0	8	US-09-641-528-22468	Sequence 22509, A
8	16	80.0	8	US-09-641-528-22509	Sequence 22509, A
9	16	80.0	8	US-09-641-528-31337	Sequence 31337, A
10	16	80.0	8	US-09-641-528-34368	Sequence 34368, A
11	16	80.0	8	US-09-641-528-35881	Sequence 35881, A
12	16	80.0	8	US-09-641-528-39670	Sequence 39670, A
13	16	80.0	8	US-09-641-528-41710	Sequence 41710, A
14	16	80.0	8	US-09-641-528-42699	Sequence 42699, A
15	16	80.0	8	US-09-641-528-44	Sequence 44, Appl
16	16	80.0	8	US-09-641-528-734	Sequence 734, Appl
17	16	80.0	8	US-09-641-528-1054	Sequence 1054, Appl
18	16	80.0	8	US-09-641-528-20273	Sequence 20273, A
19	16	80.0	8	US-09-641-528-20303	Sequence 21722, A
20	16	80.0	8	US-09-641-528-21722	Sequence 21757, A
21	16	80.0	8	US-09-641-528-22468	Sequence 22509, A
22	16	80.0	8	US-09-641-528-22509	Sequence 22509, A
23	16	80.0	8	US-09-641-528-31337	Sequence 31337, A
24	16	80.0	8	US-09-641-528-34368	Sequence 34368, A
25	16	80.0	8	US-09-641-528-35881	Sequence 35881, A
26	16	80.0	8	US-09-641-528-39670	Sequence 39670, A

27	16	80.0	8	US-09-641-528-35881	Sequence 35881, A
28	16	80.0	8	US-09-641-528-39670	Sequence 39670, A
29	16	80.0	8	US-09-641-528-41710	Sequence 41710, A
30	16	80.0	8	US-09-641-528-42699	Sequence 42699, A
31	16	80.0	9	US-09-641-528-11581	Sequence 11581, A
32	16	80.0	9	US-09-641-528-13540	Sequence 13540, A
33	16	80.0	9	US-09-641-528-14770	Sequence 14770, A
34	16	80.0	9	US-09-641-528-17935	Sequence 17935, A
35	16	80.0	9	US-09-641-528-18786	Sequence 18786, A
36	16	80.0	9	US-09-641-528-19183	Sequence 19183, A
37	16	80.0	9	US-09-641-528-31569	Sequence 31569, A
38	16	80.0	9	US-09-641-528-34605	Sequence 34605, A
39	16	80.0	9	US-09-641-528-36102	Sequence 36102, A
40	16	80.0	9	US-09-641-528-39626	Sequence 39626, A
41	16	80.0	9	US-09-641-528-41874	Sequence 41874, A
42	16	80.0	9	US-09-641-528-42842	Sequence 42842, A
43	16	80.0	9	US-09-641-528-45197	Sequence 45197, A
44	16	80.0	9	US-09-641-528-45626	Sequence 45626, A
45	16	80.0	9	US-09-641-528-45830	Sequence 45830, A

ALIGNMENTS

```

RESULT 1
US-09-641-528-44
; Sequence 44, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-44
Query Match      80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 FXXXW 5
Db 4 FSRW 8
RESULT 2
US-09-641-528-734
; Sequence 734, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001

```

```
;; CURRENT APPLICATION NUMBER: US/09/641,528
;; CURRENT FILING DATE: 2000-08-15
;; PRIOR APPLICATION NUMBER: US 60/172,705
;; PRIOR FILING DATE: 1999-12-10
;; NUMBER OF SEQ ID NOS: 51504
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO: 734
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-734
```

```
Query Match      80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 FXXXW 5
   | |
Db 4 FSRTW 8
```

```
RESULT 3
US-09-641-528-1054
; Sequence 1054, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 1054
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-1054
```

```
Query Match      80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 FXXXW 5
   | |
Db 4 FSRTW 8
```

```
RESULT 4
US-09-641-528-20273
; Sequence 20273, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
```

```
;; CURRENT FILING DATE: 2000-08-15
;; PRIOR APPLICATION NUMBER: US 60/172,705
;; PRIOR FILING DATE: 1999-12-10
;; NUMBER OF SEQ ID NOS: 51504
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO: 20273
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-20273
```

```
Query Match      80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 FXXXW 5
   | |
Db 4 FSRTW 5
```

```
RESULT 5
US-09-641-528-20303
; Sequence 20303, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 20303
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-20303
```

```
Query Match      80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 FXXXW 5
   | |
Db 4 FSRTW 8
```

```
RESULT 6
US-09-641-528-21722
; Sequence 21722, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
```

;; PRIOR APPLICATION NUMBER: US 60/172,705
;; PRIOR FILING DATE: 1999-12-10
;; NUMBER OF SEQ ID NOS: 51504
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 21722
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-21722

Query Match 80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
| |
DB 1 FSRTW 5

RESULT 7
US-09-641-528-21757
;; Sequence 21757, Application US/09641528
;; GENERAL INFORMATION:
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Celis, Esteban
;; APPLICANT: Grey, Howard
;; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;; FILE REFERENCE: 2060.0100001
;; CURRENT APPLICATION NUMBER: US/09/641,528
;; CURRENT FILING DATE: 2000-08-15
;; PRIOR APPLICATION NUMBER: US 60/172,705
;; PRIOR FILING DATE: 1999-12-10
;; NUMBER OF SEQ ID NOS: 51504
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 21757
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-21757

Query Match 80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
| |
DB 4 FSRTW 8

RESULT 8
US-09-641-528-22468
;; Sequence 22468, Application US/09641528
;; GENERAL INFORMATION:
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Celis, Esteban
;; APPLICANT: Grey, Howard
;; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;; FILE REFERENCE: 2060.0100001
;; CURRENT APPLICATION NUMBER: US/09/641,528
;; CURRENT FILING DATE: 2000-08-15
;; PRIOR APPLICATION NUMBER: US 60/172,705

;; PRIOR FILING DATE: 1999-12-10
;; NUMBER OF SEQ ID NOS: 51504
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 22468
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-22468

Query Match 80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
| |
DB 1 FSRTW 5

RESULT 9
US-09-641-528-22509
;; Sequence 22509, Application US/09641528
;; GENERAL INFORMATION:
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Celis, Esteban
;; APPLICANT: Grey, Howard
;; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;; FILE REFERENCE: 2060.0100001
;; CURRENT APPLICATION NUMBER: US/09/641,528
;; CURRENT FILING DATE: 2000-08-15
;; PRIOR APPLICATION NUMBER: US 60/172,705
;; PRIOR FILING DATE: 1999-12-10
;; NUMBER OF SEQ ID NOS: 51504
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 22509
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-22509

Query Match 80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
| |
DB 4 FSRTW 8

RESULT 10
US-09-641-528-31337
;; Sequence 31337, Application US/09641528
;; GENERAL INFORMATION:
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Celis, Esteban
;; APPLICANT: Grey, Howard
;; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;; FILE REFERENCE: 2060.0100001
;; CURRENT APPLICATION NUMBER: US/09/641,528
;; CURRENT FILING DATE: 2000-08-15
;; PRIOR APPLICATION NUMBER: US 60/172,705
;; PRIOR FILING DATE: 1999-12-10

NUMBER OF SEQ ID NOS: 51504
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31337
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-31337

Query Match 80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 2 FSRTW 6

RESULT 11
US-09-641-528-34368
Sequence 34368, Application US/09641528
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51504
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34368
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-34368

Query Match 80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 2 FSRTW 6

RESULT 12
US-09-641-528-35881
Sequence 35881, Application US/09641528
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51504

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35881
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-35881

Query Match 80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 2 FSRTW 6

RESULT 13
US-09-641-528-39670
Sequence 39670, Application US/09641528
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51504
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 39670
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-39670

Query Match 80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 2 FSRTW 6

RESULT 14
US-09-641-528-41710
Sequence 41710, Application US/09641528
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51504
SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 41710
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-41710

```

```

Query Match      80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Oy 1 FXXW 5
   1
Db 2 FSRTW 6

```

```

RESULT 15
US-09-641-528-42699
; Sequence 42699, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42699
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-42699

```

```

Query Match      80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Oy 1 FXXW 5
   1
Db 2 FSRTW 6

```

Search completed: January 29, 2003, 14:21:05
Job time : 18 secs

10

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:16:08 : Search time 14 Seconds
(without alignments)
10,508 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXW 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 132970

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	85.0	13	4	US-09-085-072-7
2	16	80.0	6	1	US-07-920-519-10
3	16	80.0	6	1	US-08-086-410-7
4	16	80.0	6	1	US-08-314-586-10
5	16	80.0	10	1	US-08-208-886C-87
6	16	80.0	10	1	US-08-704-744-89
7	16	80.0	10	1	US-08-469-557-68
8	16	80.0	10	2	US-08-290-793B-68
9	16	80.0	11	1	US-08-277-660A-16
10	16	80.0	11	1	US-08-277-660A-17
11	16	80.0	11	1	US-08-424-957-29
12	16	80.0	11	1	US-08-424-957-30
13	16	80.0	11	4	US-09-035-686-29
14	16	80.0	11	4	US-09-035-686-30
15	16	80.0	12	2	US-08-406-330-32
16	16	80.0	12	2	US-08-556-597-32
17	16	80.0	13	1	US-08-305-871A-23
18	16	80.0	13	3	US-08-912-560-11
19	16	80.0	13	4	US-08-788-822A-27
20	16	80.0	13	6	5185431-25
21	16	80.0	15	1	US-08-218-025A-139
22	16	80.0	15	4	US-08-847-844A-22
23	16	80.0	15	5	PCT-US93-08699-1
24	16	80.0	16	4	US-09-330-914A-11
25	16	80.0	17	1	US-08-218-025A-115
26	16	80.0	17	2	US-08-746-283-7
27	16	80.0	17	2	US-08-746-257A-5

28	16	80.0	17	3	US-08-987-743-11	Sequence 11, Appl
29	16	80.0	18	2	US-08-934-913-125	Sequence 125, App
30	16	80.0	18	3	US-08-513-968-40	Sequence 40, App
31	16	80.0	18	4	US-09-025-769B-249	Sequence 249, App
32	16	80.0	20	1	US-08-218-025A-64	Sequence 64, Appl
33	16	80.0	20	1	US-08-493-235-31	Sequence 65, Appl
34	16	80.0	20	2	US-08-162-934-19	Sequence 31, Appl
35	16	80.0	20	4	US-09-162-934-19	Sequence 19, Appl
36	15	75.0	6	1	US-08-277-660A-2	Sequence 2, Appl1
37	15	75.0	6	1	US-08-424-957-2	Sequence 3, Appl1
38	15	75.0	6	1	US-08-424-957-3	Sequence 2, Appl1
39	15	75.0	6	1	US-08-424-957-6	Sequence 6, Appl1
40	15	75.0	6	1	US-09-035-686-2	Sequence 2, Appl1
41	15	75.0	6	4	US-09-035-686-3	Sequence 3, Appl1
42	15	75.0	6	4	US-09-035-686-6	Sequence 6, Appl1
43	15	75.0	6	4	US-09-081-975-1	Sequence 1, Appl1
44	15	75.0	7	1	US-08-358-160-189	Sequence 189, App
45	15	75.0				

ALIGNMENTS

RESULT 1
US-09-085-072-7
Sequence 7, Application US/09085072
Patent No. 6265150
GENERAL INFORMATION:
APPLICANT: L. Tetslappen et al.
TITLE OF INVENTION: PHAGE ANTIBODIES
NUMBER OF INVENTIONS: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Barton, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: USA
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,072
FILING DATE: 26-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: 890-2 FWC/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-085-072-7
Query Match 85.0%; Score 17; DB 4; Length 13;
Best Local Similarity 40.0%; Pred. No. 8 7e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 FXXW 5
Db 6 FASW 10

RESULT 2

US-07-920-519-10
; Sequence 10, Application US/07920519
; Patent No. 5382518
; GENERAL INFORMATION:
; APPLICANT: CAPUT, DANIEL
; APPLICANT: FERRARA, PASCUAL
; APPLICANT: GUILLEMOT, JEAN-CLAUDE
; APPLICANT: KAGHAD, MOURAD
; APPLICANT: LEGOUX, RICHARD
; APPLICANT: LOISON, GERARD
; APPLICANT: LABRE, ELIZABETH
; APPLICANT: LUKER, JOHANNES
; APPLICANT: LEPLATOIS, PASCUAL
; APPLICANT: SALOME, MARK
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,
; TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/920,519
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/659,408
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16781/276 BEDL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; IMMEDIATE SOURCE:
; CLONE: Hydrolysis product T 23
; US-07-920-519-10

Query Match 80.0%; Score 16; DB 1; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 1 FDATA 5

RESULT 3
US-08-086-410-7
; Sequence 7, Application US/08086410
; Patent No. 5407822
; GENERAL INFORMATION:
; APPLICANT: LEPLATOIS, PASCUAL
; APPLICANT: LOISON, Gerard
; APPLICANT: 3

APPLICANT: PESSEQUE, Bernard
; APPLICANT: SHIRE, David
; TITLE OF INVENTION: Artificial promoter for the expression
; TITLE OF INVENTION: of proteins in yeast
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: King Street Station, Suite 500, 1800 Diagonal
; STREET: Road, PO Box 299
; CITY: ALEXANDRIA
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086,410
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,083
; FILING DATE: 02-OCT-1991
; APPLICATION NUMBER: FR 89 17467
; FILING DATE: 29-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: SAYE, Bernard D
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/318
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: hydrolysis product T23
; US-08-086-410-7

Query Match 80.0%; Score 16; DB 1; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 1 FDATA 5

RESULT 4
US-08-314-586-10
; Sequence 10, Application US/08314586
; Patent No. 5541098
; GENERAL INFORMATION:
; APPLICANT: CAPUT, DANIEL
; APPLICANT: FERRARA, PASCUAL
; APPLICANT: GUILLEMOT, JEAN-CLAUDE
; APPLICANT: KAGHAD, MOURAD
; APPLICANT: LEGOUX, RICHARD
; APPLICANT: LOISON, GERARD
; APPLICANT: LABRE, ELIZABETH
; APPLICANT: LUKER, JOHANNES
; APPLICANT: LEPLATOIS, PASCUAL
; APPLICANT: SALOME, MARK
; APPLICANT: LAURENT, PATRICK
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,
; TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
; MICROORGANISMS AND TRANSFORMED CELLS

NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,586
FILING DATE: 28-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/659,408
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16781/509/BDL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
IMMEDIATE SOURCE:
CLONE: Hydrolysis product T 23
US-08-314-586-10

Query Match 80.0%; Score 16; DB 1; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
1 1
Db 1 FDATAW 5

RESULT 5
US-08-208-886C-87
Sequence 87, Application US/08208886C
Patent No. 5597710
GENERAL INFORMATION:
APPLICANT: Dallee, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/208,886C
FILING DATE: March 10, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298 2987
TELEFAX: 908 298 5388
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-208-886C-87

Query Match 80.0%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
1 1
Db 4 FSSW 8

RESULT 6
US-08-704-744-89
Sequence 89, Application US/08704744
Patent No. 5705154
GENERAL INFORMATION:
APPLICANT: Dallee, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,744
FILING DATE: 06-SEPT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208886
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: PCT/US/95/02400
FILING DATE: 08-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2987
TELEFAX: (908) 298-5388
TELEX:
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-74-89

Query Match 80.0%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
Dk 4 FSSYW 8

RESULT 7
US-08-469-557-68
Sequence 68, Application US/08469557
Patent No. 5770403
GENERAL INFORMATION:

APPLICANT: Daille, Barbara

APPLICANT: Le, Hung

APPLICANT: Miller, Kenneth

APPLICANT: Murgolo, Nicholas

APPLICANT: Nguyen, Hanh

APPLICANT: Tindall, Stephen

APPLICANT: Zavodny, Paul

TITLE OF INVENTION: Cloning and Expression of

TITLE OF INVENTION: Humanized Monoclonal Antibodies

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schering-Plough Corporation

STREET: 2000 Galloping Hill Road

CITY: Kenilworth

STATE: New Jersey

COUNTRY: USA

ZIP: 07033-0530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 6.0.5

SOFTWARE: Microsoft Word 5.1A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,557

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/290,793

FILING DATE: August 16, 1994

APPLICATION NUMBER: PCT/US93/01301

FILING DATE: 19-FEB-1992

APPLICATION NUMBER: US 07/841,659

FILING DATE: 19-FEB-1992

APPLICATION NUMBER: US 07/782,784

FILING DATE: 24-OCT-1991

APPLICATION NUMBER: US 07/499,327

FILING DATE: 21-MAY-1990

APPLICATION NUMBER: PCT/US88/03631

FILING DATE: 21-OCT-1988

APPLICATION NUMBER: US 07/655,966

FILING DATE: 14-FEB-1991

APPLICATION NUMBER: US 07/113,623

FILING DATE: 26-OCT-1987

APPLICATION NUMBER: US 06/881,553

FILING DATE: 03-JUL-1986

APPLICATION NUMBER: US 06/843,958

FILING DATE: 25-MAR-1986

APPLICATION NUMBER: US 06/799,668

FILING DATE: 19-NOV-1985

ATTORNEY/AGENT INFORMATION:

NAME: Foulke, Cynthia L.

REGISTRATION NUMBER: 32,364

REFERENCE/DOCKET NUMBER: 2409K7

TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ. ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-557-68

Query Match 80.0%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
Dk 4 FSSYW 8

RESULT 8
US-08-290-793B-68
Sequence 68, Application US/08290793B
Patent No. 5863537
GENERAL INFORMATION:

APPLICANT: Daille, Barbara

APPLICANT: Le, Hung

APPLICANT: Miller, Kenneth

APPLICANT: Murgolo, Nicholas

APPLICANT: Nguyen, Hanh

APPLICANT: Tindall, Stephen

APPLICANT: Zavodny, Paul

TITLE OF INVENTION: Cloning and Expression of

TITLE OF INVENTION: Humanized Monoclonal Antibodies

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schering-Plough Corporation

STREET: 2000 Galloping Hill Road

CITY: Kenilworth

STATE: New Jersey

COUNTRY: USA

ZIP: 07033-0530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 6.0.5

SOFTWARE: Microsoft Word 5.1A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290,793B

FILING DATE: August 16, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/01301

FILING DATE: 19-FEB-1992

APPLICATION NUMBER: US 07/841,659

FILING DATE: 19-FEB-1992

APPLICATION NUMBER: US 07/782,784

FILING DATE: 24-OCT-1991

APPLICATION NUMBER: US 07/499,327

FILING DATE: 21-MAY-1990

APPLICATION NUMBER: PCT/US88/03631

FILING DATE: 21-OCT-1988

APPLICATION NUMBER: US 07/655,966

FILING DATE: 14-FEB-1991

APPLICATION NUMBER: US 07/113,623

FILING DATE: 26-OCT-1987

APPLICATION NUMBER: US 06/881,553

FILING DATE: 03-JUL-1986

APPLICATION NUMBER: US 06/843,958

FILING DATE: 25-MAR-1986

APPLICATION NUMBER: US 06/799,668

FILING DATE: 19-NOV-1985

ATTORNEY/AGENT INFORMATION:

NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: 2409K7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-290-793B-68

Query Match 80.0%; Score 16; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXW 5
1
DB 4 FSSW 8

RESULT 9
US-08-277-660A-16
Sequence 16, Application US/08277660A
Patent No. 5702908
GENERAL INFORMATION:
APPLICANT: Picklesley, Steven M.
APPLICANT: Lane, David P.
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
TITLE OF INVENTION: Protein and Therapeutic Application Thereof
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,660A
FILING DATE: 20-JUL-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-60244/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
US-08-277-660A-16

Query Match 80.0%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXW 5
1
DB 5 FSAW 9

RESULT 10
US-08-277-660A-17
Sequence 17, Application US/08277660A
Patent No. 5702908
GENERAL INFORMATION:
APPLICANT: Picklesley, Steven M.
APPLICANT: Lane, David P.
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
TITLE OF INVENTION: Protein and Therapeutic Application Thereof
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,660A
FILING DATE: 20-JUL-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-60244/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
US-08-277-660A-17

Query Match 80.0%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXW 5
1
DB 5 FSDW 9

RESULT 11
US-08-424-957-29
Sequence 29, Application US/08424957
Patent No. 5770377
GENERAL INFORMATION:
APPLICANT: Picklesley, Steven M.
APPLICANT: Lane, David P.
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
TITLE OF INVENTION: Protein and Therapeutic Application Thereof
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,957
FILING DATE: 19-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,660
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-61228/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-424-957-29

Query Match 80.0%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 5 FSAW 9

RESULT 12
US-08-424-957-30
Sequence 30, Application US/08424957
Patent No. 5770377
GENERAL INFORMATION:
APPLICANT: Picketsley, Steven M.
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
TITLE OF INVENTION: Protein and Therapeutic Application Thereof
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,957
FILING DATE: 19-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,660
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-61228/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-424-957-30

Query Match 80.0%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 5 FSDW 9

RESULT 13
US-09-035-686-29
Sequence 29, Application US/09035686
Patent No. 6153391
GENERAL INFORMATION:
APPLICANT: Picketsley, Steven M.
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
TITLE OF INVENTION: Protein and Therapeutic Application Thereof
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,686
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/424,957
FILING DATE: 19-APR-1995
APPLICATION NUMBER: US 08/277,660
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-61228/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-09-035-686-29

Query Match 80.0%; Score 16; DB 4; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 5 FSAW 9

RESULT 14
US-09-035-686-30
Sequence 30, Application US/09035686

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; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Pickstley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDK2 and P53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-09-035-686-30

Query Match      80.0%; Score 16; DB 4; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
   1 1
DB 5 FSDAW 9

RESULT 15
US-08-406-330-32
; Sequence 32, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN 1b/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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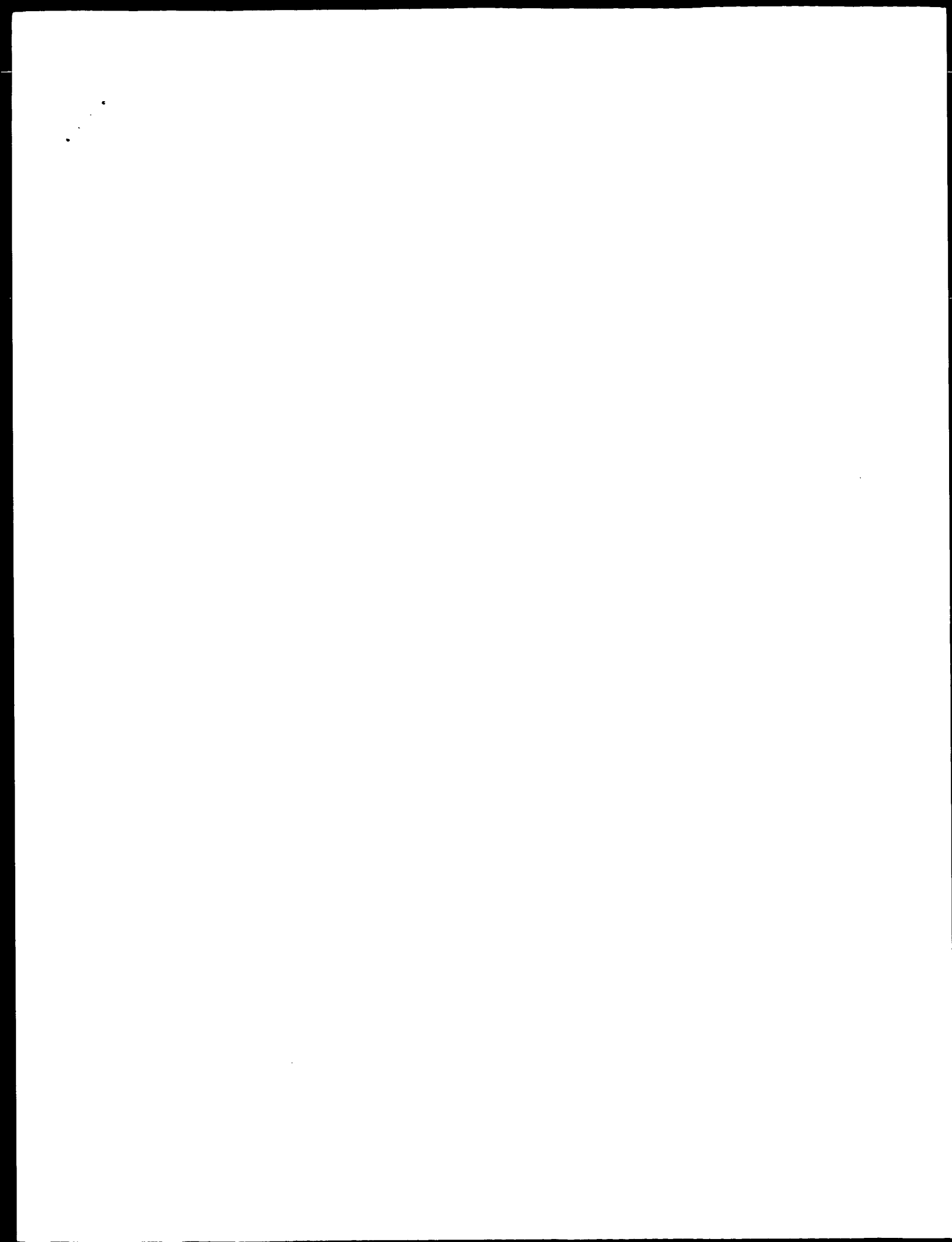
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-406-330-32

Query Match      80.0%; Score 16; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
   1 1
DB 3 FSSW 7

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Search completed: January 29, 2003, 14:18:21
 Job time : 15 secs



RESULT 3
JH0253
gut pentapeptide - Japanese eel
C:Species: Anguilla japonica (Japanese eel)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C:Accession: JH0253
R:Jesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A:Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A:Reference number: JH0253; MUID:92062113; PMID:1953755
A:Accession: JH0253
A:Molecule type: protein
A:Residues: 1-5 <UES>
A:Experimental source: gut
A:Title: This peptide increased basal tone of the circular muscle of the esophagogastric, and of the circular muscle of the gastro-intestinal junction.

Query Match 55.0%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
|
DB 3 W 3

RESULT 4
G37196
bradykinin-potentiating peptide 7 - island jararaca
C:Species: Bothrops insularis (Island jararaca)
C>Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: G37196
R:Cintrra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides
A:Reference number: A37196; MUID:90351557; PMID:2386615
A:Accession: G37196
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <CTN>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 55.0%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
|
DB 3 W 3

RESULT 5
PT0281
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0281
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0281
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 55.0%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
|
DB 4 W 4

RESULT 6
PT0308
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0308
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0308
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 55.0%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
|
DB 2 W 2

RESULT 7
PT0729
T-cell receptor beta chain V-D-J region (120-1J) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0640; PT0685; PT0729
R:Reaney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0640
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>
A:Experimental source: newborn thymus, strain BALB/c, clone 120-1J
A:Accession: PT0685
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE2>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C
A:Accession: PT0729
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE3>
A:Experimental source: newborn thymus, strain BALB/c, clone 135-1AG
C:Keywords: T-cell receptor

Query Match 55.0%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
|
DB 5 W 5

RESULT 8
PT0580
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0580

R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0580
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <PE>
 A:Experimental source: day 19 fetal thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 55.0%; Score 11; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
 |
 Db 4 W 4

RESULT 9
 A44955
 alkalal monooxygenase (PMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragment)
 C:Species: Vibrio harveyi
 C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
 C:Accession: A44955
 R:Paquette, O.; Tu, S.C.
 Photochem. Photobiol. 50, 817-825, 1989
 A:Title: Chemical modification and characterization of the alpha cysteine 106 at the Vth
 A:Reference number: A44955; MUID:90157500; PMID:2626493
 A:Accession: A44955
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <PAQ>
 C:Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 30.0%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 |
 Db 1 F 1

RESULT 10
 S70615
 endo-1,4-beta-xylanase (EC 3.2.1.8) - Streptomyces sp. (Chainia sp. NCL 82.5.1) (fragment)
 N:Alternate names: xylanase
 C:Species: Streptomyces sp.
 A:Variety: Chainia sp. NCL 82.5.1
 C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
 C:Accession: S70615
 R:Rao, M.; Khadilkar, S.; Bandivadekar, K.R.; Deshpande, V.
 Biochem. J. 316, 771-775, 1996
 A:Title: Structural environment of an essential cysteine residue of xylanase from Chainia
 A:Reference number: S70615; MUID:96265041; PMID:8670151
 A:Accession: S70615
 A:Molecule type: protein
 A:Residues: 1-5 <RAO>
 A:Experimental source: Chainia sp. strain NCL 82.5.1
 A:Note: the source is designated as Chainia sp.
 C:Function:
 A:Description: endohydrolyzation of beta-1,4-xylosidic linkages in xylans
 A:Pathway: fermentation of hemicellulose into ethanol
 C:Keywords: glycosidase; hydrolase

Query Match 30.0%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 |

Db 3 F 3

RESULT 11
 PS0324
 ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)
 C:Species: Oryza sativa (rice)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998
 C:Accession: PS0324
 R:Tsuigita, A.
 submitted to JIPID, April 1993
 A:Reference number: PS0206
 A:Accession: PS0324
 A:Molecule type: protein
 A:Residues: 1-5 <TSU>
 A:Experimental source: leaf, chlorophyll

Query Match 30.0%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 |
 Db 1 F 1

RESULT 12
 B45525
 actin I - malaria parasite (Plasmodium falciparum) (fragments)
 C:Species: Plasmodium falciparum
 C:Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
 C:Accession: B45525
 R:Wessling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoen
 Mol. Biochem. Parasitol. 35, 167-176, 1989
 A:Title: Stage-specific expression and genomic organization of the actin genes of the
 A:Reference number: B45525; MUID:89364966; PMID:2671721
 A:Accession: B45525
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-5 <WES>
 A:Cross-references: GB:J03988
 A:Note: the authors translated the codon GAA for residue 3 as Gly
 C:Comment: The actin I gene contains no introns.

Query Match 30.0%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 |
 Db 5 F 5

RESULT 13
 A44692
 fulcin - giant African snail
 C:Species: Achatina fulica (giant African snail)
 C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
 C:Accession: A44692
 R:Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.;
 Blochem. Biophys. Res. Commun. 178, 486-493, 1991
 A:Title: Fulcin, a novel neurotoxic peptide containing a D-amino acid residue isolated fro
 A:Reference number: A44692; MUID:91315471; PMID:1859408
 A:Accession: A44692
 A:Molecule type: protein
 A:Residues: 1-5 <OHT>
 C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide
 F:2/Modified site: D-asparagine (Asn) #status experimental
 F:5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 30.0%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
|
Db 1 F 1

RESULT 14

B61445
Leu-enkephalin - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C:Accession: B61445
R:Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis
A:Reference number: A61445; MID:84144823; PMID:6583690
A:Accession: B61445
A:Molecule type: protein
A:Residues: 1-5 <LEU>
A:Experimental source: pedal ganglia
C:Keywords: neuropeptide; opioid peptide

Query Match 30.0%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
|
Db 4 F 4

RESULT 15

A61445
Met-enkephalin - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C:Accession: A61445
R:Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis
A:Reference number: A61445; MID:84144823; PMID:6583690
A:Accession: A61445
A:Molecule type: protein
A:Residues: 1-5 <LEU>
A:Experimental source: pedal ganglia
C:Keywords: neuropeptide; opioid peptide

Query Match 30.0%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
|
Db 4 F 4

Search completed: January 29, 2003, 14:23:17
Job time : 14 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2003, 14:18:23 ; Search time 11 Seconds
(without alignments)
18.853 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20

Sequence: 1 FXXXW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	55.0	5	1 BPP7_BOTIN	P30425 bothrops in
2	11	55.0	5	1 UP01_MOUSE	P83639 mus musculu
3	6	30.0	5	1 AL14_CARMA	P81817 carcinus ma
4	6	30.0	5	1 EI03_LITRU	P82099 litorea rub
5	6	30.0	5	1 EI04_LITRU	P82100 litorea rub
6	6	30.0	5	1 FARP_ARTTR	P41853 artiposthi
7	6	30.0	5	1 PAP2_PARMA	P81864 pardachilus
8	6	30.0	5	1 RP11_LITRU	P82070 litorea rub
9	6	30.0	5	1 RE21_LITRU	P82071 litorea rub
10	6	30.0	5	1 UP01_MOUSE	P82072 litorea rub
11	6	30.0	5	1 RE32_LITRU	P82073 litorea rub
12	6	30.0	5	1 SUGA_ACHDO	P19991 acheta dome
13	6	30.0	5	1 TPIS_CANPA	P43714 canis fami
14	6	30.0	5	1 UC22_MATZE	P80628 zea mays (m
15	3	15.0	5	1 PRC2_PERRAM	P01373 periplaneta
16	3	15.0	5	1 PSK_DAUCA	P8261 daucus caro
17	0	0.0	5	1 BIOA_CITFR	P13071 citrobacter
18	0	0.0	5	1 BIOB_CITFR	P12997 citrobacter
19	0	0.0	5	1 TRM3_ECOLI	P13973 escherichia
20	0	0.0	5	1 UXA4_CHLTR	P38005 chlamydia t

ALIGNMENTS

RESULT 1

BPP7_BOTIN STANDARD: PRT: 5 AA.
P30425;
01-APR-1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting

DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;

RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990).
CC -I- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR: G37196; G37196.
KW Hypotensive agent; Venom.
FT MOD_RES 1
SQ SEQUENCE 5 AA: 629 MW: 776DC37326B00000 CRC64;

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
Db 3 W 3

RESULT 2

UP01_MOUSE STANDARD: PRT: 5 AA.
P38639;
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -I- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 19 KDa.
FT NON_TER 5
SQ SEQUENCE 5 AA: 717 MW: 7364087043100000 CRC64;
Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

AL14_CARMA STANDARD: PRT: 5 AA.
P81817;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)

DE Carcinustatin 14.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=67559;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -i- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -i- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 5 5 AMIDATION (POTENTIAL).
 SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.le+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
 DB 3 F 3

RESULT 4
 EIO3_LITRU STANDARD; PRT; 5 AA.
 AC P82099;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Electricin 3.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -i- SUBCELLULAR LOCATION: SECRETED.
 KW Amphibian skin; Amidation.
 FT MOD_RES 5 5 AMIDATION.
 SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.le+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
 DB 1 F 1

RESULT 5
 EIO4_LITRU STANDARD; PRT; 5 AA.
 ID EIO4_LITRU
 AC P82100;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Electricin 4.

OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -i- SUBCELLULAR LOCATION: SECRETED.
 KW Amphibian skin; Amidation.
 FT MOD_RES 5 5 AMIDATION.
 SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.le+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
 DB 1 F 1

RESULT 6
 FARP_ARTTR STANDARD; PRT; 5 AA.
 ID FARP_ARTTR
 AC P41853;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide RYIRF-amide.
 OS Arthropoda; Metazoa; Platylaelminthes; Turbellaria; Sericata; Tricladida;
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Sericata; Tricladida;
 OC Terricola; Geoplanidae; Arthurdendyus.
 OX NCBI_TaxID=132421;
 RN [1]
 RP SEQUENCE AND SYNTHESIS.
 RX MEDLINE=94211927; PubMed=7909164;
 RA Maule A.G., Shaw C., Hallon D.W., Curry W.J., Thim L.;
 RT "RYIRFamide: a turbellarian FMRFamide-related peptide (FARP).";
 RL Regul. Pept. 50:37-43(1994).
 CC -i- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 5 5 AMIDATION.
 SQ SEQUENCE 5 AA; 754 MW; 69D4004B44600000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.le+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
 DB 5 F 5

RESULT 7
 PAP2_PARMA STANDARD; PRT; 5 AA.
 ID PAP2_PARMA
 AC P81864;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pardaxin II (PXII) (Fragment).
 OS Pardaxinus marmoratus (Red sea moles sole).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Soleoidei; Soleidae; Pardachirus.

OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic polypeptides from the secretion of the Red sea moses sole (Parachanna marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -1- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
CC -1- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A Tetramer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KM Toxin.
FT NON TER
SQ SEQUENCE 5 AA: 614 MW; 7769C9C9C8100000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
DB 2 F 2

RESULT 8
RE31_LITRU
ID RE31_LITRU STANDARD; PRT: 5 AA.
AC P82070;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rubellidin 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C., Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog 'Litoria rubella', the skin peptide profile as a probe for the study of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KM Amphibian skin.
SQ SEQUENCE 5 AA: 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
DB 3 F 3

RESULT 9
RE21_LITRU
ID RE21_LITRU STANDARD; PRT: 5 AA.
AC P82071;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rubellidin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C., Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog 'Litoria rubella', the skin peptide profile as a probe for the study of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KM Amphibian skin.
SQ SEQUENCE 5 AA: 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
DB 3 F 3

RESULT 10
RE31_LITRU
ID RE31_LITRU STANDARD; PRT: 5 AA.
AC P82072;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C., Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog 'Litoria rubella', the skin peptide profile as a probe for the study of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KM Amphibian skin; Amidation.
FT MOD RES 5
SQ SEQUENCE 5 AA: 656 MW; 71A9C9CA10300000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
DB 3 F 3

RESULT 11
RE32_LITRU

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ID RE32_LITRU STANDARD: PRT: 5 AA.
AC P82073;
DE 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wapnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -I- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC ACTIVITY.
CC -I- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW Amphibian skin.
SQ SEQUENCE 5 AA: 570 MW: 71A9C9C862A00000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 3 F 3

RESULT 12
SUGA_ACHDO STANDARD: PRT: 5 AA.
ID SUGA_ACHDO
AC P19991;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Suboesophageal ganglion pentapeptide.
OS Acheta domestica (House cricket).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera;
OC Gryllidae; Gryllinae; Acheta.
NCBI_TaxID=6997;
RN [1]
RP SEQUENCE.
RA Wicker C., Wicker C.;
RT "Isolation and structure of a peptide isolated from the
RT suboesophageal ganglion of Acheta domestica (orthoptera).";
RL Comp. Biochem. Physiol. 88C:185-187(1987)
CC -I- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
CC GANGLIA.
DR PIR: JS0319;
SQ SEQUENCE 5 AA: 476 MW: 69D76DDDD800000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 5 F 5

RESULT 13
TPIS_CANFA STANDARD: PRT: 5 AA.
ID TPIS_CANFA
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

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DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
GN TPIL.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RA MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins."
RL Electrophoresis 18:2795-2802(1997).
CC -I- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate -> glycero-
CC phosphate.
CC -I- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR HSC-2DPAGE: P54714; DOG.
DR InterPro: IPR000652; Triophos. Ismrse.
DR PROSITE: PS00121; TIM, PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 1 1
FT NON_TER 5 5
SQ SEQUENCE 5 AA: 550 MW: 64444862C9A00000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 1 F 1

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RESULT 14
UC22_MAIZE STANDARD: PRT: 5 AA.
ID UC22_MAIZE
AC P80628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of elutriated coleoptile (Spot 474)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
DR Maize2DB: P80628; COLEOPTILE.
DR Maize2DB: 123954;
FT NON_TER 1 1
FT NON_TER 5 5
SQ SEQUENCE 5 AA: 654 MW: 72CB19C9C0300000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1

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Db 2 F 2

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RESULT 15
PRCT_PERAM STANDARD: PRT: 5 AA.
AC P01373:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 01-FEB-1995 (Rel. 31, last annotation update)
DE proctolin.
OS Periplaneta americana (American cockroach).
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA staratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;
RX MEDLINE=8125865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
RN [3]
RP SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
RN [4]
RP SEQUENCE.
RC SPECIES=C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC THE CRAB PERICARDIAL ORGANS.
DR PIR: A01644; HOROHA.
DR PIR: A60411; A60411.
DR A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA: 649 MW: 7187673844600000 CRC64;

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Query Match 15.0%; Score 3; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 F 1
: 2 Y 2

Search completed: January 29, 2003, 14:22:21
Job time : 12 secs

10

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:20:44 ; Search time 28 Seconds
(without alignments)
36.794 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriap:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	30.0	5	13	P83308
2	0	0.0	5	2	P83073
3	0	0.0	5	10	Q99007

ALIGNMENTS

RESULT 1
P83308 PRELIMINARY: PRT: 5 AA.
AC P83308;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE FMRFamide-like neuropeptide (LPLRF-amide).

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-BRAIN;
RX PubMed=6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to FMRFamide."
RL Nature 305:328-330(1983).
CC -1- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide.
KW SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 30.0%; Score 6; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
DB 5 F 5

RESULT 2

P83073 PRELIMINARY: PRT: 5 AA.
AC P83073;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE 88 kDa protein (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 11796;
RA Browne N., Dowds B.C.A.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
FT NON TER 5
SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 6.7e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 F 1
DB 1 M 1

RESULT 3

Q99007 PRELIMINARY: PRT: 5 AA.
AC Q99007;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1) (Fragment).
GN AMY1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=HIMALAYA; TISSUE-ALEURONE LAYER;
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimeric genes by gibberellic
RT acid and abscisic acid in protoplasts prepared from mature barley
RT aleurone layers.";
RL Plant Mol. Biol. 16:713-721(1991).
CC -I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -I- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -I- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC BARLEY.
DR EMBL; X54643; CAA38455.1; .
KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.
FT NON_PEP 5 5
SQ SEQUENCE 5 AA; 600 MW; 61E334DD6F00000 CRC64;

Query Match 0.0%; Score 0; DB 10; Length 5;
Best Local Similarity 0.0%; Pred. No. 6.7e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 F 1
DB 1 M 1

Search completed: January 29, 2003, 14:22:55
Job time : 28 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:18:03 ; Search time 34 Seconds
(without alignments)
19.596 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 13629

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
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15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	75.0	5	17	AAW17807
2	15	75.0	5	17	AAW17812
3	15	75.0	5	17	AAW17806
4	15	75.0	5	20	AAV33038
5	15	75.0	5	21	AAW07280
6	14	70.0	5	13	AAW26471
7	14	70.0	5	13	AAW26473
8	14	70.0	5	13	AAW29438
9	14	70.0	5	13	AAW29448
10	14	70.0	5	15	AAW47436

11	14	70.0	5	15	AAW69220	Endothelin C-termi
12	14	70.0	5	15	AAW69260	Endothelin C-termi
13	14	70.0	5	15	AAW69210	Endothelin C-termi
14	14	70.0	5	16	AAW89837	Melanotrophic rele
15	14	70.0	5	16	AAW89842	Melanotrophic rele
16	14	70.0	5	17	AAW17808	Cyclic pentapeptid
17	14	70.0	5	17	AAW17809	Cyclic pentapeptid
18	14	70.0	5	17	AAW89811	p33/MDM2 binding 1
19	14	70.0	5	17	AAW89812	p33/MDM2 binding 1
20	14	70.0	5	18	AAW22914	Low density lipopr
21	14	70.0	5	19	AAW78939	Antidepressant MIF
22	14	70.0	5	19	AAW78938	Antidepressant MIF
23	14	70.0	5	19	AAW50861	Cyclic peptide whi
24	14	70.0	5	20	AAV14091	Affinity ligand fo
25	14	70.0	5	20	AAV17477	Antidepressant age
26	14	70.0	5	21	AAV58280	Human p53 consensu
27	14	70.0	5	23	AAO20822	Hydrophobic interna
28	13	65.0	5	6	AAW50708	Hexapeptide somato
29	13	65.0	5	16	AAW89838	Melanotrophic rele
30	13	65.0	5	16	AAW89840	Melanotrophic rele
31	13	65.0	5	16	AAW89841	Melanotrophic rele
32	13	65.0	5	16	AAW89843	Melanotrophic rele
33	13	65.0	5	16	AAW89828	Melanotrophic rele
34	13	65.0	5	16	AAW89829	Melanotrophic rele
35	13	65.0	5	16	AAW89830	Melanotrophic rele
36	13	65.0	5	16	AAW89831	Melanotrophic rele
37	13	65.0	5	16	AAW89832	Melanotrophic rele
38	13	65.0	5	16	AAW89833	Melanotrophic rele
39	13	65.0	5	16	AAW89834	Melanotrophic rele
40	13	65.0	5	16	AAW89835	Melanotrophic rele
41	13	65.0	5	16	AAW89836	Melanotrophic rele
42	13	65.0	5	16	AAW89839	Melanotrophic rele
43	13	65.0	5	16	AAW89818	Melanotrophic rele
44	13	65.0	5	16	AAW89820	Melanotrophic rele
45	13	65.0	5	16	AAW89821	Melanotrophic rele

ALIGNMENTS

RESULT 1	
AAW17807	
ID	AAW17807 standard; peptide; 5 AA.
XX	
AC	AAW17807:
XX	
DT	07-JUL-1997 (first entry)
XX	
DE	Cyclic pentapeptide #23 used in LH-RH receptor antagonist.
XX	
KW	Luteinising hormone releasing hormone receptor; LH-RH; antagonist;
KW	sex-hormone; human; veterinary medicine; cancer; prostate; uterus;
KW	breast; pituitary; prostatic; endometriosis; hysteromyoma;
KW	precocious puberty; amenorrhoea; premenstrual syndrome; cyclic;
KW	multilocular ovarian syndrome; comedo; pregnancy; contraception;
KW	ovulation; menstrual cycle; oestrus; meat quality; growth; spawning;
KW	fish; testosterone; superagonist; leuporelin acetate.
XX	
Key	
FT	Location/Qualifiers
FT	Modified-site 1
FT	/note= "joined via a peptide linkage to Trp5"
FT	Modified-site 2
FT	/note= "Opt. N-pToluenesulphonylarginine, D-form residue"
FT	Modified-site 3
FT	/label= Nal
FT	Misc-difference 4
FT	/note= "D-form residue"
FT	Modified-site 5
FT	/note= "joined via a peptide linkage to Phe1"
XX	Synthetic.
XX	

```

PN W09634012-A1.
XX 31-OCT-1996.
XX
XX 25-APR-1996; 96WO-JP01140.
XX
XX 09-MAY-1995; 95JP-0110933.
XX 28-APR-1995; 95JP-0106775.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Furuya S, Kato K, Kitada C;
XX WPI; 1996-497569/49.
XX
XX Cyclic penta:peptide(s), some new, as LH-RH receptor antagonists -
XX used to treat or prevent sex hormone dependent disorders, e.g.
XX cancer, also for control of pregnancy and menstruation and to
XX improve meat quality in animals
XX
XX Example 40-41; Page 170; 198pp; English.
XX
XX This peptide represents a cyclic peptide which is included in the
XX luteinising hormone releasing hormone (LH-RH) receptor antagonist
XX composition of the invention. Peptides such as this are used to
XX prevent or treat sex-hormone dependent disorders in human or veterinary
XX medicine, esp. cancers (of the prostate, uterus, breast or pituitary),
XX prostaticomegaly, endometriosis, hysteromyoma or precocious puberty, but
XX also amenorrhoea, premenstrual syndrome, multifollicular ovarian syndrome,
XX comedo, etc.; also to control pregnancy (contraception for men or women,
XX also to induce ovulation) and the menstrual cycle. They are also used
XX to control oestrus in animals, to improve meat quality and control
XX growth, and to promote spawning in fish. They may also inhibit the
XX transient increase in testosterone blood levels caused by admin. of
XX superagonists such as leuporelin acetate.
XX
XX Sequence 5 AA:
XX
XX Query Match 75.0%; Score 15; DB 17; Length 5;
XX Best Local Similarity 60.0%; Pred. No. 7.7e+05;
XX Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 FXXXX 5
XX | | |
XX 1 FRXXW 5
XX
XX RESULT 2
XX AAW17812
XX ID AAW17812 standard; peptide: 5 AA.
XX
XX AC AAW17812;
XX
XX DT 07-JUL-1997 (first entry)
XX
XX Cyclic pentapeptide #28 used in LH-RH receptor antagonist.
XX
XX Luteinising hormone releasing hormone receptor; LH-RH; antagonist;
XX sex-hormone; human; veterinary medicine; cancer; prostate; uterus;
XX breast; pituitary; prostaticomegaly; endometriosis; hysteromyoma;
XX precocious puberty; amenorrhoea; premenstrual syndrome; cyclic;
XX multifollicular ovarian syndrome; comedo; pregnancy; contraception;
XX ovulation; menstrual cycle; oestrus; meat quality; growth; spawning;
XX fish; testosterone; superagonist; leuporelin acetate.
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX /note= "Joined via a peptide linkage to Trp5"
XX Modified-site 2
XX /note= "N-piroluenesulphonylarginine, D-form residue"
XX Modified-site 3
XX /label= OTHER
XX /note= "Parafluorophenylalanine"
XX
XX FT

```

```

FT Misc-difference 4
FT /note= "D-form residue"
FT Modified-site 5
FT /note= "Joined via a peptide linkage to Phe1"
XX
XX Synthetic.
XX
XX W09634012-A1.
XX
XX 31-OCT-1996.
XX
XX 25-APR-1996; 96WO-JP01140.
XX
XX 09-MAY-1995; 95JP-0110933.
XX 28-APR-1995; 95JP-0106775.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Furuya S, Kato K, Kitada C;
XX WPI; 1996-497569/49.
XX
XX Cyclic penta:peptide(s), some new, as LH-RH receptor antagonists -
XX used to treat or prevent sex hormone dependent disorders, e.g.
XX cancer, also for control of pregnancy and menstruation and to
XX improve meat quality in animals
XX
XX Example 50; Page 176; 198pp; English.
XX
XX This peptide represents a cyclic peptide which is included in the
XX luteinising hormone releasing hormone (LH-RH) receptor antagonist
XX composition of the invention. Peptides such as this are used to
XX prevent or treat sex-hormone dependent disorders in human or veterinary
XX medicine, esp. cancers (of the prostate, uterus, breast or pituitary),
XX prostaticomegaly, endometriosis, hysteromyoma or precocious puberty, but
XX also amenorrhoea, premenstrual syndrome, multifollicular ovarian syndrome,
XX comedo, etc.; also to control pregnancy (contraception for men or women,
XX also to induce ovulation) and the menstrual cycle. They are also used
XX to control oestrus in animals, to improve meat quality and control
XX growth, and to promote spawning in fish. They may also inhibit the
XX transient increase in testosterone blood levels caused by admin. of
XX superagonists such as leuporelin acetate.
XX
XX Sequence 5 AA:
XX
XX Query Match 75.0%; Score 15; DB 17; Length 5;
XX Best Local Similarity 60.0%; Pred. No. 7.7e+05;
XX Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 FXXXX 5
XX | | |
XX 1 FRXXW 5
XX
XX RESULT 3
XX AAW17806
XX ID AAW17806 standard; peptide: 5 AA.
XX
XX AC AAW17806;
XX
XX DT 07-JUL-1997 (first entry)
XX
XX Cyclic pentapeptide #22 used in LH-RH receptor antagonist.
XX
XX Luteinising hormone releasing hormone receptor; LH-RH; antagonist;
XX sex-hormone; human; veterinary medicine; cancer; prostate; uterus;
XX breast; pituitary; prostaticomegaly; endometriosis; hysteromyoma;
XX precocious puberty; amenorrhoea; premenstrual syndrome; cyclic;
XX multifollicular ovarian syndrome; comedo; pregnancy; contraception;
XX ovulation; menstrual cycle; oestrus; meat quality; growth; spawning;
XX fish; testosterone; superagonist; leuporelin acetate.
XX
XX Key Location/Qualifiers
XX
XX FT

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```

FT Modified-site 1 /note= "Joined via a peptide linkage to Trp5, opt.
FT /note= "parachlorophenylalanine"
FT Misc-difference 2 /note= "opt. N-(4-methoxy-2,3,6-trimethylbenzene-
FT sulphonyl)arginine, Arg, N-propionylsulphonyl]-
FT arginine, opt. D-form residue"
FT Modified-site 3 note= "opt. parachlorophenylalanine"
FT Misc-difference 4 /note= "D-form residue"
FT Modified-site 5 /note= "Joined via a peptide linkage to Phe1"
FT
FT
FT Synthetic.
FT
FT WO9634012-A1.
FT
FT 31-OCT-1996.
FT
FT 25-APR-1996; 96WO-JP01140.
FT
FT 09-MAY-1995; 95JP-0110933.
FT
FT 28-APR-1995; 95JP-0106775.
FT
FT (TAKE ) TAKEDA CHEM IND LTD.
FT
FT Furuya S, Kato K, Kltada C;
FT
FT WPI; 1996-497569/49.
FT
FT Cyclic penta-peptide(s), some new, as LH-RH receptor antagonists -
FT used to treat or prevent sex hormone dependent disorders, e.g.
FT cancer, also for control of pregnancy and menstruation and to
FT improve meat quality in animals
FT
FT
FT Example 33-39, 42-43 and 47; Page 167; 198pp; English.
FT
FT
FT This peptide represents a cyclic peptide which is included in the
FT luteinizing hormone releasing hormone (LH-RH) receptor antagonist
FT composition of the invention. Peptides such as this are used to
FT prevent or treat sex-hormone dependent disorders in human or veterinary
FT medicine, esp. cancers (of the prostate, uterus, breast or pituitary),
FT prostaticmegaly, endometriosis, hysteromyoma or precocious puberty, but
FT also amenorrhoea, premenstrual syndrome, multilocular ovarian syndrome,
FT Comedo, etc.; also to control pregnancy (contraception for men or women,
FT also to induce ovulation) and the menstrual cycle. They are also used
FT to control oestrus in animals, to improve meat quality and control
FT growth, and to promote spawning in fish. They may also inhibit the
FT transient increase in testosterone blood levels caused by admin. of
FT superagonists such as leuporelin acetate.
FT
FT
FT Sequence 5 AA:
SO

```

Query Match 75.0%; Score 15; DB 17; Length 5;
 Best Local Similarity 40.0%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 FXXXM 5
DB 1 FRFAW 5

```

RESULT 4
 AAY33038 standard; peptide; 5 AA.
 AAY33038;
 03-NOV-1999 (first entry)
 Carbohydrate antigen peptide mimotope 11.

```

KW Mimotope; antigen; carbohydrate; antibody; mimic; vaccine; adjuvant;
KW Tumour immunity; cancer therapy; antibacterial; immune response;
KW Immunogenicity; anti-idiotype; T cell response manipulation.
OS Synthetic.
PN WO9940433-A1.
PD 12-AUG-1999.
PF 04-FEB-1999; 99WO-US02405.
PR 04-FEB-1998; 98US-0073690.
PA (UYPE-) UNIV PENNSYLVANIA.
PI Kieber-Emmons T;
DR WPI; 1999-527317/44.
PT Peptides and recombinant antibody mimics of carbohydrate antigens,
PT used for, e.g. treatment of cancer and infection
PS Claim 21; Page 72; 86pp; English.
XX
XX This invention describes a novel method for preparing a peptide or
XX recombinant antibody, which mimics an antigenic carbohydrate. The
XX peptides and recombinant antibodies prepared to mimic antigenic
XX carbohydrates can be used to enhance binding of anti-antigenic
XX carbohydrate antibodies to the antigenic carbohydrate, e.g. as vaccine
XX adjuvants. The peptides can be used to inhibit binding of a ligand to a
XX receptor, which is an antigenic carbohydrate. The methods are used to
XX prepare the peptides and antigenic antibodies, which mimic the antigenic
XX carbohydrates. Carbohydrate-conjugate vaccines could be used in tumour
XX immunity and cancer therapy. The peptides and antibodies can also be
XX used as antibacterials. Peptides that mimic carbohydrate antigens can be
XX formulated to develop a longer lasting immune response. Other advantages
XX of the peptide mimics are: (1) the chemical composition and purity of
XX synthesized peptides can be precisely defined; (2) the immunogenicity
XX of the peptides can be significantly enhanced by polymerization or
XX addition of relatively small carrier molecules that reduce the total
XX amount of antigen required for immunization; (3) peptide synthesis may
XX be more practical than synthesis of carbohydrate-protein conjugates or
XX the production of anti-idiotypes; (4) peptide mimicking sequences can
XX be engineered into DNA plasmids for DNA vaccination to further
XX manipulate T cell responses. AAY33028-Y33087 represent the carbohydrate
XX antigen peptide mimotopes described in the invention.
SO

```

Query Match 75.0%; Score 15; DB 20; Length 5;
 Best Local Similarity 40.0%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 FXXXM 5
DB 1 FSLW 5

```

RESULT 5
 AAB07280 standard; peptide; 5 AA.
 AAB07280;
 17-OCT-2000 (first entry)
 Motif binding to anti-Lewis antigen antibody BR55-2.
 Human; peptide-mimetic; tumour metastasis; E-selectin;
 adhesion molecule; Lewis antigen; anti-adhesion therapy.
 OS Unidentified.

XX WO200027420-A1.
 PN 18-MAY-2000.
 XX
 PD 05-NOV-1999; 99WO-US26277.
 XX
 PF 06-NOV-1998; 98US-0107478.
 XX
 PR (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Blaszczyk-Thurin M, Kieber-Edmons T;
 XX WPI: 2000-376309/32.
 DR
 PT Peptidomimetics of carbohydrate Lewis ligands useful for modulating
 PT inflammation, metastasis and angiogenesis -
 XX
 PS Example 5; Page 37; 107pp; English.
 XX
 CC Tumour metastasis requires detachment of malignant cells from the primary
 CC tumour, penetration of blood or lymph vessels and attachment to the
 CC endothelium of distant organs, ultimately resulting in the formation of
 CC new tumours. The selectin family of adhesion molecules is implicated in
 CC this process. E-selectin is a calcium-dependent molecule expressed by
 CC activated vascular endothelium. E-selectins bind to glycoconjugates
 CC carrying a terminal tetrasaccharide Lewis antigen, which are found on
 CC tumour cell surfaces. One such Lewis antigen is Lewis X (LeX). The
 CC binding of selectin molecules to their ligands is thought to be an
 CC E-selectin-dependent carbohydrate-mediated interaction of
 CC be a target for anti-cancer therapy. The present sequence is thought to
 CC planar-X-planar type motif. This motif is thought to bind to anti-LeX
 CC antibody BR55-2. BR55-2 is a peptido-mimetics of E-selectins. Peptides
 CC that block E-selectin-LeX binding and therefore adhesion of tumour cells
 CC and leukocytes to endothelial cells inhibit metastasis.
 XX
 SQ Sequence 5 AA;
 XX
 QY Query Match 75.0%; Score 15; DB 21; Length 5;
 DB Best Local Similarity 40.0%; Pred. No. 7.7e+05;
 1 FSLW 5 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 6
 AAR26471
 ID AAR26471 standard; peptide; 5 AA.
 XX
 AC AAR26471;
 XX
 DT 22-OCT-1992 (first entry)
 XX
 DE Serotonin release inhibitor peptide.
 XX
 KM Ganglion: konaganishi; tortoise roll shell; nervous; muscular;
 KM system; neurotransmitter; psychotropic; circulatory; drug.
 XX
 OS Tortoise roll shell.
 XX
 PN JP04091096-A.
 XX
 PD 24-MAR-1992.
 XX
 PF 02-APR-1990; 90JP-0087827.
 XX
 PR 02-APR-1990; 90JP-0087827.
 XX
 PA (SUNR) SUNTORY LTD.

XX WPI: 1992-148003/18.
 DR
 XX
 PT New glycyL-tryptophan and oligopeptide(s) contg. it - esp.
 PT alanyl-prolyl deriv., as serotonin release inhibitor for
 PT psychotropic and circulatory agent, and control of mono:amine or
 PT peptide neuro-transmitter
 XX
 PS Claim 1; Page 1; 10pp; Japanese.
 XX
 CC The peptide (or forms of it truncated from the N-terminus) was prepd.
 CC by extraction from ganglion of konaganishi (tortoise roll shell)
 CC with organic solvent, adsorption chromatography and gel filtration.
 CC The oligopeptide is a useful reagent in biology or medical science
 CC relating to the physiology of the nervous muscular system. It can
 CC also be used for controlling monoamine or peptide neurotransmitter
 CC relating reactions (e.g. inhibiting serotonin release) and as a
 CC psychotropic or circulatory drug.
 XX
 SQ Sequence 5 AA;
 XX
 QY Query Match 70.0%; Score 14; DB 13; Length 5;
 DB Best Local Similarity 40.0%; Pred. No. 7.7e+05;
 1 FARGW 5 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 7
 AAR26473
 ID AAR26473 standard; peptide; 5 AA.
 XX
 AC AAR26473;
 XX
 DT 22-OCT-1992 (first entry)
 XX
 DE Serotonin release inhibitor peptide.
 XX
 KM Ganglion: konaganishi; tortoise roll shell; nervous; muscular;
 KM system; neurotransmitter; psychotropic; circulatory; drug.
 XX
 OS Tortoise roll shell.
 XX
 PN JP04091096-A.
 XX
 PD 24-MAR-1992.
 XX
 PF 02-APR-1990; 90JP-0087827.
 XX
 PR 02-APR-1990; 90JP-0087827.
 XX
 PA (SUNR) SUNTORY LTD.
 XX
 DR WPI: 1992-148003/18.
 XX
 PT New glycyL-tryptophan and oligopeptide(s) contg. it - esp.
 PT alanyl-prolyl deriv., as serotonin release inhibitor for
 PT psychotropic and circulatory agent, and control of mono:amine or
 PT peptide neuro-transmitter
 XX
 PS Claim 1; Page 1; 10pp; Japanese.
 XX
 CC The peptide (or forms of it truncated from the N-terminus) was prepd.
 CC by extraction from ganglion of konaganishi (tortoise roll shell)
 CC with organic solvent, adsorption chromatography and gel filtration.
 CC The oligopeptide is a useful reagent in biology or medical science
 CC relating to the physiology of the nervous muscular system. It can
 CC also be used for controlling monoamine or peptide neurotransmitter
 CC relating reactions (e.g. inhibiting serotonin release) and as a
 CC psychotropic or circulatory drug.

CC See also AAR26471-3.

XX Sequence 5 AA:

Query Match 70.0%; Score 14; DB 13; Length 5;
Best Local Similarity 40.0%; Pred. No. 7.7e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
1 FSPGW 5

RESULT 8
AAR29438
ID AAR29438 standard; peptide: 5 AA.

XX AAR29438;

XX 13-APR-1993 (first entry)

XX Endothelin antagonist peptide.

XX Hypertension; myocardial infarction; congestive heart failure;
KW endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;
KW acute renal failure; preeclampsia; diabetes; metabolic;
KW endocrinological; neurological; disorders.

XX Synthetic.

XX Key Location/Qualifiers
FT Modified-site 1 /note=" (Ac- or 1-adamantyl acetic acid) - D-Phe"

XX W09220706-A.

XX 26-NOV-1992.

XX 24-APR-1992; 92MO-US03408.

XX 16-MAY-1991; 91US-0701274.

XX 18-DEC-1991; 91US-0809746.

XX (WARN) WARNER LAMBERT CO.

XX Cody WL, Depue P, Doherty AM, Taylor MD;

XX WPI: 1992-415706/50.

XX New peptide(s) used as endothelin antagonists - for treating
PT hypertension, metabolic and endocrine disorders, heart failure,
PT diabetes, asthma, neurological disorders, etc.

XX Claim 5; Page 94; 116pp: English.

XX The peptide is an endothelin antagonist useful in controlling
CC hypertension, myocardial infarction, congestive heart failure,
CC endotoxic shock, subarachnoid haemorrhage, asthma, arrhythmias,
CC acute renal failure, preeclampsia, diabetes and metabolic,
CC endocrinological and neurological disorders. Administration is oral
CC parenteral or by inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/
CC day. It may be prepared by conventional peptide synthesis.

XX Sequence 5 AA:

Query Match 70.0%; Score 14; DB 13; Length 5;
Best Local Similarity 40.0%; Pred. No. 7.7e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
1 FDIW 5

RESULT 9
AAR29448
ID AAR29448 standard; peptide: 5 AA.

XX AAR29448;

XX 13-APR-1993 (first entry)

XX Endothelin antagonist peptide.

XX Hypertension; myocardial infarction; congestive heart failure;
KW endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;
KW acute renal failure; preeclampsia; diabetes; metabolic;
KW endocrinological; neurological; disorders.

XX Synthetic.

XX Key Location/Qualifiers
FT Modified-site 1 /note="Ac-D-Phe"

XX W09220706-A.

XX 26-NOV-1992.

XX 24-APR-1992; 92MO-US03408.

XX 16-MAY-1991; 91US-0701274.

XX 18-DEC-1991; 91US-0809746.

XX (WARN) WARNER LAMBERT CO.

XX Cody WL, Depue P, Doherty AM, Taylor MD;

XX WPI: 1992-415706/50.

XX New peptide(s) used as endothelin antagonists - for treating
PT hypertension, metabolic and endocrine disorders, heart failure,
PT diabetes, asthma, neurological disorders, etc.

XX Claim 5; Page 95; 116pp: English.

XX The peptide is an endothelin antagonist useful in controlling
CC hypertension, myocardial infarction, congestive heart failure,
CC endotoxic shock, subarachnoid haemorrhage, asthma, arrhythmias,
CC acute renal failure, preeclampsia, diabetes and metabolic,
CC endocrinological and neurological disorders. Administration is oral
CC parenteral or by inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/
CC day. It may be prepared by conventional peptide synthesis.

XX Sequence 5 AA:

Query Match 70.0%; Score 14; DB 13; Length 5;
Best Local Similarity 40.0%; Pred. No. 7.7e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
1 FDIW 5

RESULT 10
AAR47436
ID AAR47436 standard; peptide: 5 AA.

XX AAR47436;

XX 30-JUN-1994 (first entry)

XX Cyclic peptide which modulates endothelin activity.

XX Cyclic peptide; endothelin; inhibitor; receptor; detection;

KW isolation; antagonist; hypertension; pulmonary hypertension;
 KW cardiovascular disease; bronchoconstriction; asthma;
 KW inflammatory disease; ophthalmologic shock; anaphylactic shock;
 KW hemorrhagic shock; gastroenteric disease; renal failure;
 KW endotoxin shock; menstrual disorders; obstetric conditions;
 KW erythropoietin-mediated vasoconstriction; wound treatment.
 XX
 FH Key
 F1 Misc-difference 1 Location/Qualifiers
 F1 /note= "D-Tyr bonded to D-Trp at position 5."
 F1 Misc-difference 3
 F1 /label= D-Ala.
 F1 Misc-difference 5
 F1 /note= "D-Trp bonded to D-Tyr at position 1."
 XX
 PA W09325580-A.
 XX
 XX 23-DEC-1993.
 XX
 PF 17-JUN-1993; 93WO-US05788.
 XX
 PF 18-JUN-1992; 92US-0900620.
 PF 18-JUN-1992; 92US-0900711.
 XX
 PA (IMMU-) IMMUNOPHARMACEUTICS INC.
 XX
 PI Balaji VN, Chan MF;
 XX WPI; 1994-007458/01.
 DR
 XX New cyclic peptide(s) which modulate endothelin activity - used
 PT for treating endothelin-mediated disorders such as cardiovascular
 PT and respiratory diseases
 XX
 PS Claim 2; Page 51; 58pp; English.
 XX
 CC The peptide inhibits binding of endothelin-1 (ET) to ETA receptors
 CC and/or to ETB receptors. It can be used for detecting,
 CC distinguishing and isolating ET receptor subtypes. The peptides
 CC also act as ET antagonists and can be used to treat endothelin-
 CC mediated disorders such as hypertension, pulmonary hypertension,
 CC cardiovascular disease, bronchoconstriction, asthma, inflammatory
 CC diseases, ophthalmologic shock, anaphylactic shock, hemorrhagic
 CC shock, gastroenteric disease, renal failure, endotoxin shock,
 CC menstrual disorders, obstetric conditions, erythropoietin-mediated
 CC vasoconstriction and wounds.
 CC
 SO Sequence 5 AA:
 Query Match 70.0%; Score 14; DB 15; Length 5;
 Best Local Similarity 20.0%; Pred. NO. 7.7e+05;
 Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 1
 DB 1 YAAAW 5
 RESULT 11
 AAR69220
 ID AAR69220 standard; peptide; 5 AA.
 XX
 AC AAR69220;
 XX
 DT 06-MAR-1995 (first entry)
 XX
 DE Endothelin C-terminal peptide analog, useful as antagonist.
 XX
 KW Endothelin; ET-1; receptor; antagonist.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers

FT Misc-difference 1 /note= "Ac-D-Phe"
 FT
 XX
 XX W09414843-A.
 PN
 XX 07-JUL-1994.
 PD
 XX
 XX 17-DEC-1993; 93WO-US12377.
 PF
 XX
 PR 21-DEC-1992; 92US-0995480.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Cody WL, Depue P, Doherty AM, He JX, Taylor MD;
 XX WPI; 1994-234617/28.
 DR
 XX
 PT New hexapeptide derivs. inhibiting endothelin - for treatment of
 PT e.g. renal failure, hypertension, asthma, restenosis, angina,
 PT cancer etc.
 XX
 PS Claim 5; Page 119; 146pp; English.
 XX
 CC Novel antagonists of endothelin are claimed which are C-terminal
 CC hexapeptides and analogs of ET-1. The first (N-terminal) amino acid
 CC of the new peptides has D-configuration. The peptides are claimed
 CC generically. The present peptide is a specifically claimed example
 CC of the generic compounds.
 CC The peptides are useful for treating hypertension, metabolic and
 CC endocrine disorders, congestive heart failure, myocardial infarction,
 CC endotoxic shock, subarachnoid haemorrhage, arrhythmia, asthma, acute
 CC and chronic renal failure, preclampsia, diabetes, neurological
 CC disorders, pulmonary hypertension, ischemic disease, ischemic bowel
 CC disease, gastric mucosal damage, Raynaud's disease, restenosis,
 CC percutaneous transluminal coronary angioplasty, angina and cancer.
 CC
 SO Sequence 5 AA:
 Query Match 70.0%; Score 14; DB 15; Length 5;
 Best Local Similarity 40.0%; Pred. NO. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 1
 DB 1 FLDIW 5
 RESULT 12
 AAR69260
 ID AAR69260 standard; peptide; 5 AA.
 XX
 AC AAR69260;
 XX
 DT 07-MAR-1995 (first entry)
 XX
 DE Endothelin C-terminal peptide analog, useful as antagonist.
 XX
 KW Endothelin; ET-1; receptor; antagonist.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Ac-D-Phe"
 FT
 XX
 PA W09414843-A.
 XX
 PD 07-JUL-1994.
 XX
 PF 17-DEC-1993; 93WO-US12377.
 PF
 PR 21-DEC-1992; 92US-0995480.
 XX

CC AAR89786-R89858 are small peptide compounds based on the tripeptide
 CC hormone melanotrophic release inhibiting factor (MIF), also known as
 CC L-propyl L-leucyl glycine and melanocyte stimulating inhibitory
 CC factor. The peptides are used for treating depression and can be
 CC administered so as to achieve a circulating plasma level of 30-90 mg
 CC per average human adult. The peptides show greater anti-depressant
 CC activity than MIF. They can be administered at lower dosage than
 CC known anti-depressants which reduces potential deleterious side
 CC effects.

XX Sequence 5 AA:
 SQ

Query Match 70.0%; Score 14; DB 16; Length 5;
 Best Local Similarity 60.0%; Pred. No. 7.7e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXXW 5
 DB 1 FXIGW 5

RESULT 15
 AAR89842
 ID AAR89842 standard; peptide; 5 AA.
 AC AAR89842;
 XX
 DT 24-JUN-1996 (first entry)
 XX
 DE Melanotrophic release inhibiting factor (MIF) modified peptide analogue.
 XX
 KM MIF; melanotrophic release inhibiting factor; modified; analogue;
 KW hormone; depression; low dosage; L-propyl L-leucyl glycine;
 XX melanocyte stimulating inhibitory factor.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /label= OTHER
 FT /note= "4-F-Phe"
 FT Modified-site 2 /label= OTHER
 FT /note= "Homo-Pro"
 FT Modified-site 5 /label= OTHER
 FT /note= "amidated"
 XX
 XX W09530430-A1.
 XX
 XX 16-NOV-1995.
 XX
 XX 02-MAY-1995; 95WO-US05560.
 XX
 XX 04-MAY-1994; 94US-0238089.
 XX
 XX (INNA-) INNAPHARMA INC.
 XX
 XX Abajian HB, Hlavka JJ, Noble JF;
 XX
 XX WPT; 1995-403936/51.
 DR
 XX
 XX New tri-, tetra-, penta- and poly-peptide cpds. - based on the
 PT tri-peptide hormone melanocyte stimulating inhibitory factor, used
 PT for treating depression
 PS
 PS Claim 68; Page 32; 138pp; English.
 XX
 CC AAR89786-R89858 are small peptide compounds based on the tripeptide
 CC hormone melanotrophic release inhibiting factor (MIF), also known as
 CC L-propyl L-leucyl glycine and melanocyte stimulating inhibitory
 CC factor. The peptides are used for treating depression and can be
 CC administered so as to achieve a circulating plasma level of 30-90 mg

CC per average human adult. The peptides show greater anti-depressant
 CC activity than MIF. They can be administered at lower dosage than
 CC known anti-depressants which reduces potential deleterious side
 CC effects.

XX Sequence 5 AA:
 SQ

Query Match 70.0%; Score 14; DB 16; Length 5;
 Best Local Similarity 60.0%; Pred. No. 7.7e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXXW 5
 DB 1 FXRGW 5

Search completed: January 29, 2003, 14:22:04
 Job time : 35 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:22:59 ; Search time 10 Seconds

(without alignments)
10.089 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20

Sequence: 1 FXXHW 5

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 2031

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	70.0	5	10	US-09-214-371-2
2	14	70.0	5	10	US-09-281-717-3
3	11	55.0	5	8	US-08-239-765B-4
4	11	55.0	5	8	US-08-484-409-35
5	11	55.0	5	8	US-08-424-550B-228
6	11	55.0	5	8	US-08-424-550B-469
7	11	55.0	5	9	US-09-995-749A-14
8	11	55.0	5	9	US-09-764-884-2
9	11	55.0	5	9	US-09-895-593-15
10	11	55.0	5	9	US-09-895-593-16
11	11	55.0	5	9	US-09-423-800-62
12	11	55.0	5	9	US-09-764-857-2
13	11	55.0	5	9	US-09-860-670-2
14	11	55.0	5	9	US-09-968-561A-211
15	11	55.0	5	9	US-09-968-561A-217
16	11	55.0	5	9	US-09-981-876-2
17	11	55.0	5	9	US-09-984-245-2
18	11	55.0	5	9	US-09-764-868-2
19	11	55.0	5	9	US-10-014-485A-79

20	11	55.0	5	9	US-10-104-019-42	Sequence 42, Appl
21	11	55.0	5	9	US-09-764-904-2	Sequence 2, Appl
22	11	55.0	5	9	US-09-852-797-2	Sequence 2, Appl
23	11	55.0	5	9	US-09-964-992A-11	Sequence 11, Appl
24	11	55.0	5	9	US-10-035-349-2	Sequence 8, Appl
25	11	55.0	5	9	US-10-035-349-8	Sequence 2, Appl
26	11	55.0	5	9	US-09-828-272A-6	Sequence 6, Appl
27	11	55.0	5	9	US-10-042-141-2	Sequence 2, Appl
28	11	55.0	5	9	US-10-059-749-57	Sequence 57, Appl
29	11	55.0	5	9	US-10-059-749-63	Sequence 57, Appl
30	11	55.0	5	9	US-10-059-749-69	Sequence 69, Appl
31	11	55.0	5	9	US-10-079-625-6	Sequence 6, Appl
32	11	55.0	5	9	US-10-029-301-4	Sequence 6, Appl
33	11	55.0	5	9	US-10-074-956-6	Sequence 6, Appl
34	11	55.0	5	9	US-10-078-059-5	Sequence 5, Appl
35	11	55.0	5	9	US-10-087-195-3	Sequence 3, Appl
36	11	55.0	5	9	US-09-320-713-14	Sequence 14, Appl
37	11	55.0	5	9	US-09-774-639-2	Sequence 7, Appl
38	11	55.0	5	9	US-09-798-889-2	Sequence 2, Appl
39	11	55.0	5	9	US-09-201-396-7	Sequence 2, Appl
40	11	55.0	5	9	US-10-105-930-21	Sequence 21, Appl
41	11	55.0	5	9	US-10-105-930-57	Sequence 57, Appl
42	11	55.0	5	9	US-10-105-930-58	Sequence 58, Appl
43	11	55.0	5	9	US-10-105-930-59	Sequence 59, Appl
44	11	55.0	5	9	US-10-105-930-60	Sequence 60, Appl
45	11	55.0	5	9	US-10-105-930-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-09-214-371-2
Sequence 2, Application US/09214371B
Patient No. US20010018511A1
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Botiger, Volker
APPLICANT: Picklesley, Stephen
APPLICANT: Chene, Patrick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Garcia-Echeverria, Carlos
TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-2
Query Match
Best Local Similarity 70.0%; Score 14; DB 10; Length 5;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 FXXHW 5
DB 1 FXXHW 5
RESULT 2
US-09-281-717-3
Sequence 3, Application US/09281717

```

; Patent No. US20020061539A1
; GENERAL INFORMATION:
; APPLICANT: Baxter, John D.
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletcher, Robert J.
; APPLICANT: Kushner, Peter J.
; APPLICANT: Wagner, Richard L.
; APPLICANT: West, Brian
; APPLICANT: Yamamoto, Keith R.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; TITLE OF INVENTION: COACTIVATOR BINDING
; FILE REFERENCE: US/09/281,717
; CURRENT APPLICATION NUMBER: US/09/281,717
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 60/079,956
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ. ID NOS.: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)..(3)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-281-717-3

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Query Match          70.0%; Score 14; DB 10; Length 5;
Best Local Similarity 80.0%; Pred. No. 9.9e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 FXXXW 5
    11111
DB 1 FXXLM 5

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RESULT 3
US-08-239-765B-4
; Sequence 4, Application US/08239765B
; Patent No. US20020026650A1
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalampos
; APPLICANT: Franz, Gerald H.
; APPLICANT: Loukeris, Athanasios
; TITLE OF INVENTION: Eukaryotic Transposable Element
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/239,765B
; FILING DATE: 09-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,237
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: BT92-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240

```

```

; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-239-765B-4

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Query Match          55.0%; Score 11; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 W 5
    1
DB 3 W 3

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RESULT 4
US-08-484-409-35
; Sequence 35, Application US/08484409
; Patent No. US20020076412A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Zamvil, Scott
; TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,409
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 690068.409C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-484-409-35

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Query Match          55.0%; Score 11; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 W 5
    1
DB 2 W 2

```

```

RESULT 5
US-08-424-550B-228
; Sequence 228, Application US/08424550B
; Patent No. US20020119447A1
; GENERAL INFORMATION:

```

APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAMSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUTIK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-938-2623
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 228:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-228

Query Match 55.0%; Score 11; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

OY 5 W 5
|
Db 4 W 4

RESULT 6
US-08-424-550B-469
Sequence 469, Application US/08424550B
Patent No. US20020119447A1
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAMSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUTIK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-938-2623
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 469:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-469

Query Match 55.0%; Score 11; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

OY 5 W 5
|
Db 5 W 5

RESULT 7
US-09-995-749A-14
Sequence 14, Application US/09995749A
Patent No. US20020155568A1
GENERAL INFORMATION:
APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LOBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
FILE REFERENCE: BO43388-CIP
CURRENT APPLICATION NUMBER: US/09/995,749A
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: EPO 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 5
TYPE: PRT
ORGANISM: Neisseria polysaccharea
US-09-995-749A-14

Query Match 55.0%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

OY 5 W 5
|
Db 2 W 2

RESULT 8

US-09-764-884-2
; Sequence 2, Application US/09764884
; Patent No. US20020161208A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT203
; CURRENT APPLICATION NUMBER: US/09/764,884
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-764-884-2

Query Match 55.0%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
1
DB 1 W 1

RESULT 9
US-09-895-593-15
; Sequence 15, Application US/09895593
; Patent No. US20020160949A1
; GENERAL INFORMATION:
; APPLICANT: Pandey, Akhilesh
; APPLICANT: Ozaki, Katsutoshi
; APPLICANT: Baumann, Heinz
; APPLICANT: Levin, Steven D.
; APPLICANT: Parr, Andrew G.
; APPLICANT: Ziegler, Steven F.
; APPLICANT: Leonard, Warren J.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
; FILE REFERENCE: 00-514-E
; CURRENT APPLICATION NUMBER: US/09/895,593
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/215,658
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Type I
; OTHER INFORMATION: cytokine receptor conserved motif
; NAME/KEY: UNSURE
; LOCATION: (3)
; OTHER INFORMATION: "Xaa" can be any naturally occurring amino acid
US-09-895-593-15

Query Match 55.0%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
1
DB 1 W 1

RESULT 10
US-09-895-593-16
; Sequence 16, Application US/09895593
; Patent No. US20020160949A1
; GENERAL INFORMATION:
; APPLICANT: Pandey, Akhilesh
; APPLICANT: Ozaki, Katsutoshi
; APPLICANT: Baumann, Heinz
; APPLICANT: Levin, Steven D.
; APPLICANT: Parr, Andrew G.
; APPLICANT: Ziegler, Steven F.
; APPLICANT: Leonard, Warren J.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
; FILE REFERENCE: 00-514-E
; CURRENT APPLICATION NUMBER: US/09/895,593
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/215,658
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motif
; OTHER INFORMATION: replacing type I cytokine receptor conserved motif
US-09-895-593-16

Query Match 55.0%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
1
DB 1 W 1

RESULT 11
US-09-423-800-62
; Sequence 62, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-800-62

Query Match 55.0%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 3 W 3

RESULT 12

US-09-764-857-2
; Sequence 2, Application US/09764857
; Patent No. US20020164685A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT211
; CURRENT APPLICATION NUMBER: US/09/764,857
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-764-857-2

Query Match

Best Local Similarity 100.0%; Score 11; DB 9; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
Db 1 W 1

RESULT 13

US-09-860-670-2
; Sequence 2, Application US/09860670
; Patent No. US20020165137A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA127P1
; CURRENT APPLICATION NUMBER: US/09/860,670
; PRIOR FILING DATE: 2001-05-21
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-860-670-2

Query Match

Best Local Similarity 100.0%; Score 11; DB 9; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
Db 1 W 1

RESULT 14

US-09-968-561A-211
; Sequence 211, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:

; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-211

Query Match

Best Local Similarity 100.0%; Score 11; DB 9; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
Db 5 W 5

RESULT 15

US-09-968-561A-217
; Sequence 217, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 217
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-217

Query Match

Best Local Similarity 100.0%; Score 11; DB 9; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
Db 5 W 5

Search completed: January 29, 2003, 14:26:38
Job time : 10 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2003, 14:22:09 ; Search time 131 Seconds
(without alignments)
24.608 Million cell updates/sec

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Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXW 5
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Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 42829

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Minimum DB seq length: 5
Maximum DB seq length: 5
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

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5:	/cgn2_6/ptodata/1/paa/US081.COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	15	75.0	5	1	PCT-US99-02405-11	Sequence 11, Appl
2	15	75.0	5	1	PCT-US99-06277-114	Sequence 114, App
3	15	75.0	5	20	US-09-831-558-11	Sequence 11, Appl
4	15	75.0	5	22	US-09-831-047B-114	Sequence 114, Appl
5	15	75.0	5	22	US-09-831-047C-114	Sequence 114, Appl
6	15	75.0	5	22	US-09-894-594-11	Sequence 11, Appl

7	14	70.0	5	1	PCT-US01-209669-3	Sequence 37, Appl
8	14	70.0	5	13	US-08-981-122-37	Sequence 37, Appl
9	14	70.0	5	16	US-09-214-372-2	Sequence 2, Appl
10	14	70.0	5	16	US-09-281-717-3	Sequence 1, Appl
11	14	70.0	5	18	US-09-403-440A-1	Sequence 4, Appl
12	14	70.0	5	18	US-09-403-440A-4	Sequence 3, Appl
13	14	70.0	5	20	US-09-609-361-3	Sequence 226, Appl
14	70.0	5	23	US-09-957-806A-226	Sequence 226, Appl	
15	13	65.0	5	4	US-08-064-111B-22	Sequence 22, Appl
16	13	65.0	5	8	US-08-481-896-99	Sequence 99, Appl
17	13	65.0	5	13	US-08-981-122-2	Sequence 2, Appl
18	13	65.0	5	17	US-09-392-941-83	Sequence 83, Appl
19	13	65.0	5	17	US-09-392-941A-169	Sequence 169, Appl
20	12	60.0	5	1	PCT-US02-04431-4	Sequence 4, Appl
21	12	60.0	5	1	PCT-US02-29060-84	Sequence 84, Appl
22	12	60.0	5	1	PCT-US98-22335-320	Sequence 320, Appl
23	12	60.0	5	9	US-08-591-447-32	Sequence 32, Appl
24	12	60.0	5	9	US-08-591-447A-32	Sequence 32, Appl
25	12	60.0	5	11	US-08-753-750A-39	Sequence 39, Appl
26	12	60.0	5	11	US-08-753-750A-39	Sequence 39, Appl
27	12	60.0	5	13	US-08-961-707-320	Sequence 320, Appl
28	12	60.0	5	13	US-08-961-707-320	Sequence 320, Appl
29	12	60.0	5	19	US-09-584-501A-39	Sequence 39, Appl
30	12	60.0	5	23	US-09-953-592-84	Sequence 84, Appl
31	12	60.0	5	24	US-10-052-578-320	Sequence 320, Appl
32	12	60.0	5	24	US-10-053-520-320	Sequence 320, Appl
33	12	60.0	5	26	US-10-243-613-84	Sequence 84, Appl
34	11	55.0	5	1	PCT-US00-00807-17	Sequence 17, Appl
35	11	55.0	5	1	PCT-US00-00903-2	Sequence 2, Appl
36	11	55.0	5	1	PCT-US00-01602-223	Sequence 223, Appl
37	11	55.0	5	1	PCT-US00-02041-14	Sequence 14, Appl
38	11	55.0	5	1	PCT-US00-03062-2	Sequence 2, Appl
39	11	55.0	5	1	PCT-US00-03062-2	Sequence 2, Appl
40	11	55.0	5	1	PCT-US00-05881-838	Sequence 838, Appl
41	11	55.0	5	1	PCT-US00-05882-1686	Sequence 1686, Appl
42	11	55.0	5	1	PCT-US00-05883-1548	Sequence 1548, Appl
43	11	55.0	5	1	PCT-US00-05918-888	Sequence 888, Appl
44	11	55.0	5	1	PCT-US00-05938-1882	Sequence 1882, Appl
45	11	55.0	5	1	PCT-US00-05989-920	Sequence 920, Appl

ALIGNMENTS

```

RESULT 1
PCT-US99-02405-11
: Sequence 11, Application PC/US9902405
: GENERAL INFORMATION:
: APPLICANT: Trustees of the University of Pennsylvania
: TITLE OF INVENTION: Peptide Mimotops of Carbohydrate Antigens
: FILE REFERENCE: upn3544
: CURRENT APPLICATION NUMBER: PCT/US99/02405
: CURRENT FILING DATE: 1999-02-04
: EARLIER APPLICATION NUMBER: 60/073,690
: EARLIER FILING DATE: 1998-02-04
: NUMBER OF SEQ ID NOS: 60
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 11
: LENGTH: 5
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
PCT-US99-02405-11

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Query Match	75.0%;	Score 15;	DB 1;	length 5;
Best Local Similarity	40.0%;	Pred. No.	4.2e+06;	
Matches	2;	Conservative	0;	Mismatches 3;
				Indels 0;
				Gaps 0;
QY	1	EXXXW	5	
DB	1	FSLLW	5	

RESULT 2
PCT-US99-26277-114
; Sequence 114, Application PC/TUS9926277
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of Anatomy and Biology
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Blaszczyk-Thurin, Magdalena
; APPLICANT: Kiebler-Emmons, Thomas
; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer
; FILE REFERENCE: WST93PCT
; CURRENT APPLICATION NUMBER: PCT/US99/26277
; CURRENT FILING DATE: 1999-11-05
; EARLIER APPLICATION NUMBER: 60/107,478
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Peptido-mimetic of a Lewis antigen
PCT-US99-26277-114

Query Match 75.0%; Score 15; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
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DB 1 FSLW 5

RESULT 3
US-09-601-558-11
; Sequence 11, Application US/09601558
; GENERAL INFORMATION:
; APPLICANT: Kiebler-Emmons, Thomas
; APPLICANT: The Trustees of the University of Pennsylvania
; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens
; FILE REFERENCE: UPN3567
; CURRENT APPLICATION NUMBER: US/09/601,558
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/US99/02405
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/073,690
; PRIOR FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-601-558-11

Query Match 75.0%; Score 15; DB 20; Length 5;
Best Local Similarity 40.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
DB 1 FSLW 5

RESULT 4
US-09-831-047B-114
; Sequence 114, Application US/09831047B
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of Anatomy and Biology

; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Blaszczyk-Thurin, Magdalena
; APPLICANT: Kiebler-Emmons, Thomas
; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer
; FILE REFERENCE: WST93AUSA
; CURRENT APPLICATION NUMBER: US/09/831,047B
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/107,478
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Peptido-mimetic of a Lewis antigen
US-09-831-047B-114

Query Match 75.0%; Score 15; DB 22; Length 5;
Best Local Similarity 40.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
DB 1 FSLW 5

RESULT 5
US-09-831-047C-114
; Sequence 114, Application US/09831047C
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of Anatomy and Biology
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Blaszczyk-Thurin, Magdalena
; APPLICANT: Kiebler-Emmons, Thomas
; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer
; FILE REFERENCE: WST93AUSA
; CURRENT APPLICATION NUMBER: US/09/831,047C
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/107,478
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Peptido-mimetic of a Lewis antigen
US-09-831-047C-114

Query Match 75.0%; Score 15; DB 22; Length 5;
Best Local Similarity 40.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
DB 1 FSLW 5

RESULT 6
US-09-894-594-11
; Sequence 11, Application US/09894594
; GENERAL INFORMATION:
; APPLICANT: Kiebler-Emmons, Thomas
; APPLICANT: Welner, David B.
; APPLICANT: Monzavi-Karbassi, Behjatollah
; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules E
; FILE REFERENCE: UPN-3984
; CURRENT APPLICATION NUMBER: US/09/894,594
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/601,558

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; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: PCT/US99/02405
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/073,690
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/214,517
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Novel Sequence
; US-09-494-594-11

Query Match          75.0%; Score 15; DB 22; Length 5;
Best Local Similarity 40.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 1 FSLIW 5

RESULT 7
PCT-US01-20969-3
; Sequence 3, Application PC/TUS0120969
; GENERAL INFORMATION:
; APPLICANT: GUY, RODNEY
; APPLICANT: BAXTER, JOHN
; APPLICANT: DARIMONT, BEATRICE
; APPLICANT: PENG, WEIJUN
; APPLICANT: ROBERT, FLETTERICK
; APPLICANT: PETER, KUSHNER
; APPLICANT: RICHARD, WAGNER
; APPLICANT: BRIAN, WEST
; APPLICANT: YAMAMOTO, KEITH
; APPLICANT: GEISTLINGER, TIMOTHY
; APPLICANT: ARNOLD, JAMES
; APPLICANT: KUNTZ, IRWIN
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: 9811-016-228
; CURRENT APPLICATION NUMBER: PCT/US01/20969
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/609,361
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/079,965
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: US 60/113,146
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: US09/281,717
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(3)
; OTHER INFORMATION: Xaa is any amino acid
; PCT-US01-20969-3

Query Match          70.0%; Score 14; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FXXXW 5
```

```

Db 1 FXXIW 5

RESULT 8
US-08-981-122-37
; Sequence 37, Application US/08981122A
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Ariomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122A
; PRIOR FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
; EARLIER APPLICATION NUMBER: PCT/JP96/01734
; PRIOR FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: 5
; OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-
; OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic pep
; US-08-981-122-37

Query Match          70.0%; Score 14; DB 13; Length 5;
Best Local Similarity 40.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 1 FFRW 5

RESULT 9
US-09-214-371-2
; Sequence 2, Application US/09214371B
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Botger, Volker
; APPLICANT: Pickstey, Angelica
; APPLICANT: Pickstey, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the interaction of p53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: Where Xaa may be any amino acid
; US-09-214-371-2

Query Match          70.0%; Score 14; DB 16; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.2e+06;
```

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| | | |
Db 1 FXXLW 5

RESULT 10

US-09-281-717-3
; Sequence 3, Application US/09281717
; GENERAL INFORMATION:
; APPLICANT: Baxter, John D.
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletcher, Robert J.
; APPLICANT: Kushner, Peter J.
; APPLICANT: Wagner, Richard L.
; APPLICANT: West, Brian
; APPLICANT: Yamamoto, Keith R.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: UOAL-253/02US
; CURRENT APPLICATION NUMBER: US/09/281,717
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 60/079,956
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)..(3)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-281-717-3

Query Match 70.0%; Score 14; DB 16; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| | | |
Db 1 FXXLW 5

RESULT 11

US-09-403-440A-1
; Sequence 1, Application US/09403440A
; GENERAL INFORMATION:
; APPLICANT: Lane, David Philip
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO
; FILE REFERENCE: MEMB25.001APC
; CURRENT APPLICATION NUMBER: US/09/403,440A
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: PCT/GB98/01144
; PRIOR FILING DATE: 1998-04-20
; PRIOR APPLICATION NUMBER: GB 9708092.3
; PRIOR FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This represents a consensus sequence representing
; OTHER INFORMATION: humans and mice.
; NAME/KEY: UNSURE
; LOCATION: 2, 3
; OTHER INFORMATION: Xaa = any amino acid

US-09-403-440A-1

Query Match 70.0%; Score 14; DB 18; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| | | |
Db 1 FXXLW 5

RESULT 12

US-09-403-440A-4
; Sequence 4, Application US/09403440A
; GENERAL INFORMATION:
; APPLICANT: Lane, David Philip
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO
; FILE REFERENCE: MEMB25.001APC
; CURRENT APPLICATION NUMBER: US/09/403,440A
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: PCT/GB98/01144
; PRIOR FILING DATE: 1998-04-20
; PRIOR APPLICATION NUMBER: GB 9708092.3
; PRIOR FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This represents a consensus sequence representing
; OTHER INFORMATION: humans and mice.
; NAME/KEY: UNSURE
; LOCATION: 2, 3, 4
; OTHER INFORMATION: Xaa = any amino acid
US-09-403-440A-4

Query Match 70.0%; Score 14; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| | | |
Db 1 FXXXW 5

RESULT 13

US-09-609-361-3
; Sequence 3, Application US/09609361
; GENERAL INFORMATION:
; APPLICANT: GUY, RODNEY
; APPLICANT: BAXTER, JOHN
; APPLICANT: DARIMONT, BEATRICE
; APPLICANT: FENG, WEIJUN
; APPLICANT: ROBERT, FLETTERICK
; APPLICANT: PETER, KUSHNER
; APPLICANT: RICHARD, WAGNER
; APPLICANT: BRIAN, WEST
; APPLICANT: YAMAMOTO, KEITH
; APPLICANT: ARNOLD, JAMES
; APPLICANT: KUNTZ, IRWIN
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR ACTIVITY
; FILE REFERENCE: 9811-016-999
; CURRENT APPLICATION NUMBER: US/09/609,361
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/079,965
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: US 60/113,146
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: US09/281,717

PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 3
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)..(3)
OTHER INFORMATION: Xaa is any amino acid
US-09-609-361-3

Query Match
Best Local Similarity 70.0%; Score 14; DB 20; Length 5;
Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FXXXW 5
1 FXXLW 5

RESULT 14
US-09-957-806A-226
Sequence 226, Application US/09957806A
GENERAL INFORMATION:

APPLICANT: Roggen, Erwin
APPLICANT: Ernst, Steffen
APPLICANT: Svendsen, Allan
APPLICANT: Friis, Esben
APPLICANT: Osten, Claus
TITLE OF INVENTION: PROTEIN VARIANTS HAVING MODIFIED IMMUNOGENICITY
FILE REFERENCE: 10021.204-US
CURRENT APPLICATION NUMBER: US/09/957, 806A
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 226
LENGTH: 5
TYPE: PRT
ORGANISM: Betula
US-09-957-806A-226

Query Match
Best Local Similarity 70.0%; Score 14; DB 23; Length 5;
Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
1 FXXLW 5

RESULT 15
US-08-064-111B-22

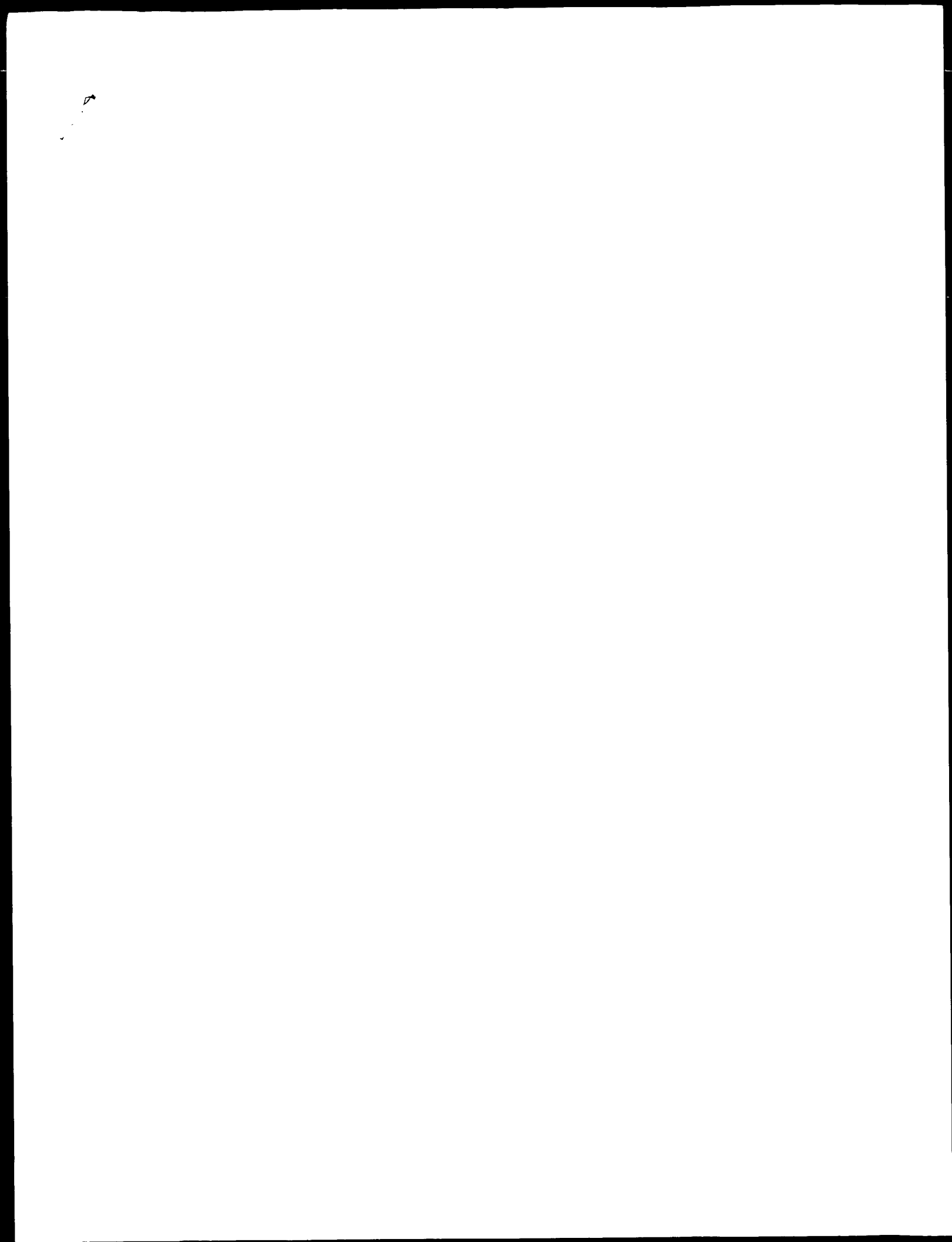
Sequence 22, Application US/08064111B
GENERAL INFORMATION:
APPLICANT: Kemp, Bruce E.
APPLICANT: Nicholson, Geoffrey C.
APPLICANT: Martin, Thomas J.
APPLICANT: Fenton, Anna J.
APPLICANT: Hammonds, R. Glenn
TITLE OF INVENTION: COMPOUNDS AND COMPOSITIONS WHICH INHIBIT
TITLE OF INVENTION: BONE RESORPTION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Aldriton & Herbert,
ADDRESS: Attn: W.H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,111B
FILING DATE: 12-AUG-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00580
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK9567
FILING DATE: 19-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK3879
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58456/MHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-064-111B-22

Query Match
Best Local Similarity 65.0%; Score 13; DB 4; Length 5;
Pred. No. 4.2e+06;
Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
1 YRSW 5

Search completed: January 29, 2003, 14:25:57
Job time: 133 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:22:24 ; Search time 18 Seconds

(without alignments)
21.950 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20

Sequence: 1 FXXXW 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 396018 seqs, 79020188 residues 1401

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	70.0	5	5	US-09-281-717A-3
2	11	55.0	5	1	PCT-US02-32657-65
3	11	55.0	5	1	PCT-US02-33556-34
4	11	55.0	5	1	PCT-US02-33556-36
5	11	55.0	5	1	PCT-US02-33556-40
6	11	55.0	5	1	PCT-US02-33985-2
7	11	55.0	5	1	PCT-US02-34760-21
8	11	55.0	5	1	PCT-US02-34760-46
9	11	55.0	5	1	PCT-US02-34760-47
10	11	55.0	5	1	PCT-US02-35606-2
11	11	55.0	5	1	PCT-US02-16525A-26
12	11	55.0	5	1	PCT-US02-24469-21
13	11	55.0	5	1	PCT-US02-24310-166
14	11	55.0	5	1	PCT-US02-24469A-21
15	11	55.0	5	1	PCT-US02-39109-15
16	11	55.0	5	1	PCT-US02-32307-23
17	11	55.0	5	1	PCT-US02-39643-5
18	11	55.0	5	4	US-08-832-443C-13
19	11	55.0	5	5	US-09-721-456-540
20	11	55.0	5	5	US-09-533-800-16
21	11	55.0	5	5	US-09-813-484-1
22	11	55.0	5	5	US-09-726-348B-5
23	11	55.0	5	5	US-09-653-812B-145
24	11	55.0	5	5	US-09-653-812B-152
25	11	55.0	5	5	US-09-556-972-12
26	11	55.0	5	5	US-09-610-650B-18

27	11	55.0	5	5	US-09-943-120-1	Sequence 1, Appl
28	11	55.0	5	5	US-09-936-759-32	Sequence 32, Appl
29	11	55.0	5	5	US-09-969-748C-19	Sequence 19, Appl
30	11	55.0	5	5	US-09-969-748C-20	Sequence 20, Appl
31	11	55.0	5	5	US-09-553-800D-16	Sequence 16, Appl
32	11	55.0	5	5	US-09-720-278A-1	Sequence 1, Appl
33	11	55.0	5	5	US-09-720-278A-2	Sequence 2, Appl
34	11	55.0	5	5	US-09-720-278A-3	Sequence 3, Appl
35	11	55.0	5	5	US-09-720-278A-5	Sequence 5, Appl
36	11	55.0	5	5	US-09-720-278A-21	Sequence 21, Appl
37	11	55.0	5	5	US-09-720-278A-23	Sequence 23, Appl
38	11	55.0	5	5	US-09-720-278A-27	Sequence 27, Appl
39	11	55.0	5	5	US-09-636-243B-30	Sequence 30, Appl
40	11	55.0	5	5	US-09-636-243B-35	Sequence 35, Appl
41	11	55.0	5	5	US-09-636-243B-44	Sequence 44, Appl
42	11	55.0	5	5	US-09-636-243B-56	Sequence 56, Appl
43	11	55.0	5	5	US-09-636-243B-57	Sequence 57, Appl
44	11	55.0	5	5	US-09-636-243B-58	Sequence 58, Appl
45	11	55.0	5	5	US-09-636-243B-59	Sequence 59, Appl

ALIGNMENTS

```
RESULT 1
US-09-281-717A-3
; Sequence 3, Application US/09281717A
; GENERAL INFORMATION:
; APPLICANT: Baxter, John
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletcher, Robert
; APPLICANT: Kushner, Peter
; APPLICANT: West, Brian
; APPLICANT: Wagner, Richard
; APPLICANT: Yamamoto, Keith
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: 9811-008-999
; CURRENT APPLICATION NUMBER: US/09/281, 717A
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/079, 956
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Variant
; LOCATION: (2)..(3)
; OTHER INFORMATION: Xaa is any amino acid
US-09-281-717A-3

Query Match          70.0%: Score 14; DB 5; Length 5;
Best Local Similarity 80.0%: Pred. No. 3e+05; 1; Indels 0;
Matches 4; Conservative 0; Mismatches 1; Gaps 0;

QY      1 FXXXW 5
DB      1 FXXXW 5

RESULT 2
PCT-US02-32657-65
; Sequence 65, Application PC/TUS0232657
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2
; FILE REFERENCE: A-801B
; CURRENT APPLICATION NUMBER: PCT/US02/32657
; CURRENT FILING DATE: 2002-10-11
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;; PRIOR APPLICATION NUMBER: US 60/414,155
;; PRIOR FILING DATE: 2002-09-27
;; PRIOR APPLICATION NUMBER: US 60/328,624
;; PRIOR FILING DATE: 2001-10-11
;; NUMBER OF SEQ ID NOS: 359
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 65
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Polypeptide capable of binding to Ang-2
PCT-US02-32857-65

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
|
DB 1 W 1

RESULT 3
PCT-US02-33556-34
;; Sequence 34, Application PC/TUS0233556
;; GENERAL INFORMATION:
;; APPLICANT: Amgen, Inc.
;; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
;; FILE REFERENCE: A-799
;; CURRENT APPLICATION NUMBER: PCT/US02/33556
;; CURRENT FILING DATE: 2002-10-17
;; NUMBER OF SEQ ID NOS: 135
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 34
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Homo sapiens
PCT-US02-33556-34

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
|
DB 4 W 4

RESULT 4
PCT-US02-33556-36
;; Sequence 36, Application PC/TUS0233556
;; GENERAL INFORMATION:
;; APPLICANT: Amgen, Inc.
;; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
;; FILE REFERENCE: A-799
;; CURRENT APPLICATION NUMBER: PCT/US02/33556
;; CURRENT FILING DATE: 2002-10-17
;; NUMBER OF SEQ ID NOS: 135
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 36
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Homo sapiens
PCT-US02-33556-36

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
|
DB 1 W 1

DB 4 W 4

RESULT 5
PCT-US02-33556-40
;; Sequence 40, Application PC/TUS0233556
;; GENERAL INFORMATION:
;; APPLICANT: Amgen, Inc.
;; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
;; FILE REFERENCE: A-799
;; CURRENT APPLICATION NUMBER: PCT/US02/33556
;; CURRENT FILING DATE: 2002-10-17
;; NUMBER OF SEQ ID NOS: 135
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 40
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Homo sapiens
PCT-US02-33556-40

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
|
DB 4 W 4

RESULT 6
PCT-US02-33985-2
;; Sequence 2, Application PC/TUS0233985
;; GENERAL INFORMATION:
;; APPLICANT: Human Genome Sciences, Inc.
;; TITLE OF INVENTION: 16 Human Secreted Proteins
;; FILE REFERENCE: PS739PCT
;; CURRENT APPLICATION NUMBER: PCT/US02/33985
;; CURRENT FILING DATE: 2002-10-24
;; PRIOR APPLICATION NUMBER: 60/330,629
;; PRIOR FILING DATE: 2001-10-26
;; NUMBER OF SEQ ID NOS: 62
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: Site
;; LOCATION: (3)
;; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
PCT-US02-33985-2

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
|
DB 1 W 1

RESULT 7
PCT-US02-34760-21
;; Sequence 21, Application PC/TUS0234760
;; GENERAL INFORMATION:
;; APPLICANT: Abbott Laboratories
;; APPLICANT: Bredley, Michael F.
;; TITLE OF INVENTION: TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES
;; TITLE OF INVENTION: HAVING ANTIANGIOGENIC ACTIVITY
;; FILE REFERENCE: 6854.WO.O1

RESULT 8
PCT-US02-34760-46
Sequence 46, Application PC/TUS0234760
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Haviv, Fortuna
TITLE OF INVENTION: TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES
FILE REFERENCE: 6854.WO.01
CURRENT APPLICATION NUMBER: PCT/US02/34760
PRIOR FILING DATE: 2002-10-30
PRIOR APPLICATION NUMBER: 10/263,811
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 10/000,540
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 10/000,007
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antiangiogenic Peptide
NAME/KEY: VARIANT
LOCATION: (2)...(2)
OTHER INFORMATION: Xaa = Nva at position 2
FEATURE:
NAME/KEY: VARIANT
LOCATION: (5)...(5)
OTHER INFORMATION: Xaa = prolylethylamide at position 5
PCT-US02-34760-21

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
|
Db 1 W 1

RESULT 9
PCT-US02-34760-47
Sequence 47, Application PC/TUS0234760
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Haviv, Fortuna
TITLE OF INVENTION: TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES
FILE REFERENCE: 6854.WO.01
CURRENT APPLICATION NUMBER: PCT/US02/34760
PRIOR FILING DATE: 2002-10-30
PRIOR APPLICATION NUMBER: 10/263,811
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 10/000,540
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 10/000,007
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 46
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antiangiogenic Peptide
NAME/KEY: VARIANT
LOCATION: (5)...(5)
OTHER INFORMATION: Xaa = proethylamide at position 5
PCT-US02-34760-46

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
|

RESULT 10
PCT-US02-35606-2
Sequence 2, Application PC/TUS0235606
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: PS740PCT
TITLE OF INVENTION: 41 Human Secreted Proteins
FILE REFERENCE: PS740PCT
CURRENT APPLICATION NUMBER: PCT/US02/35606
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/331,046
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Site
LOCATION: (3)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
PCT-US02-35606-2

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
|
Db 2 W 2

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
|

Db 1 W 1

RESULT 11

PCT-US02-16525A-26
; Sequence 26, Application PC/TUS0216525A
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16525A
; PRIORITY FILING DATE: 2002-05-24
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US02-16525A-26

Query Match

Best Local Similarity 55.0%; Score 11; DB 1; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 1 W 1

RESULT 12

PCT-US02-24469-21
; Sequence 21, Application PC/TUS0224469
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: Biological Assay Detection Method
; FILE REFERENCE: PCT 20900Y
; CURRENT APPLICATION NUMBER: PCT/US02/24469
; PRIORITY FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/310,599
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa is a variable which may be
; OTHER INFORMATION: A,R,N,D,C,Q,E,G,H,I,L,K,M,F,P,S,T,W,Y,V
; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US02-24469-21

Query Match

Best Local Similarity 55.0%; Score 11; DB 1; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 3 W 3

RESULT 13

PCT-US02-24310-166
; Sequence 166, Application PC/TUS0224310
; GENERAL INFORMATION:
; APPLICANT: CUBIST PHARMACEUTICALS, INC.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO THE DAPTOMYCIN
; FILE REFERENCE: CUB-12 PCT CIP
; CURRENT APPLICATION NUMBER: PCT/US02/24310
; PRIORITY FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US01/32354
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/310,385
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 60/379,866
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 166
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
PCT-US02-24310-166

Query Match

Best Local Similarity 55.0%; Score 11; DB 1; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 2 W 2

RESULT 14

PCT-US02-24469A-21
; Sequence 21, Application PC/TUS0224469A
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: Biological Assay Detection Method
; FILE REFERENCE: PCT 20900Y
; CURRENT APPLICATION NUMBER: PCT/US02/24469A
; PRIORITY FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/310,599
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa is a variable which may be
; OTHER INFORMATION: A,R,N,D,C,Q,E,G,H,I,L,K,M,F,P,S,T,W,Y,V
; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US02-24469A-21

Query Match

Best Local Similarity 55.0%; Score 11; DB 1; Length 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 1 W 1

Db 3 W 3

RESULT 15

PCT-US02-39109-15

: Sequence 15, Application PC/TUS0239109

: GENERAL INFORMATION:

: APPLICANT: The Government of the United States of America, as represented by the

: APPLICANT: Secretary, Department of Health and Human Services

: APPLICANT: Ruscelli, Francis W.

: APPLICANT: Ruff, Michael R.

: TITLE OF INVENTION: PEPTIDE T STIMULATES CTL RESPONSES

: FILE REFERENCE: 14014.0404P1

: CURRENT APPLICATION NUMBER: PCT/US02/39109

: CURRENT FILING DATE: 2002-12-06

: PRIOR APPLICATION NUMBER: 60/338,971

: PRIOR FILING DATE: 2001-12-07

: NUMBER OF SEQ ID NOS: 15

: SOFTWARE: FastSeq for Windows Version 4.0

: SEQ ID NO 15

: LENGTH: 5

: TYPE: PRT

: ORGANISM: Artificial Sequence

: FEATURE:

: OTHER INFORMATION: Description of Artificial Sequence:/note =

PCT-US02-39109-15

Query Match

Best Local Similarity 55.0%; Score 11; DB 1; Length 5;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5

Db 3 W 3

Search completed: January 29, 2003, 14:26:20
Job time : 18 secs

10

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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:21:29 ; Search time 14 Seconds

(without alignments)
10.508 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20

Sequence: 1 FXXXW 5

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 10533

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents.AA:*
2: /cgn2_6/plodata/1/laa/5A.COMB.pep:*
3: /cgn2_6/plodata/1/laa/5B.COMB.pep:*
4: /cgn2_6/plodata/1/laa/6A.COMB.pep:*
5: /cgn2_6/plodata/1/laa/6B.COMB.pep:*
6: /cgn2_6/plodata/1/laa/PCRUS.COMB.pep:*
7: /cgn2_6/plodata/1/laa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	70.0	5	1	US-08-424-957-4
2	14	70.0	5	1	US-08-424-957-5
3	14	70.0	5	3	US-08-981-122-37
4	14	70.0	5	4	US-09-035-686-4
5	14	70.0	5	4	US-09-035-686-5
6	14	70.0	5	4	US-09-099-053-3
7	13	65.0	5	1	US-08-064-111C-22
8	13	65.0	5	1	US-07-789-184-83
9	13	65.0	5	1	US-08-475-263-83
10	13	65.0	5	1	US-08-485-886-83
11	13	65.0	5	2	US-08-477-362-83
12	13	65.0	5	2	US-08-477-134-83
13	13	65.0	5	3	US-08-473-489A-83
14	13	65.0	5	3	US-08-485-695-83
15	13	65.0	5	3	US-08-485-695-83
16	13	65.0	5	4	US-08-981-122-2
17	11	55.0	5	1	US-07-657-769B-15
18	11	55.0	5	1	US-07-657-769B-16
19	11	55.0	5	1	US-07-657-769B-17
20	11	55.0	5	1	US-07-657-769B-18
21	11	55.0	5	1	US-07-657-769B-19
22	11	55.0	5	1	US-07-657-769B-20
23	11	55.0	5	1	US-07-657-769B-21
24	11	55.0	5	1	US-07-657-769B-22
25	11	55.0	5	1	US-07-657-769B-36
26	11	55.0	5	1	US-07-657-769B-37
27	11	55.0	5	1	US-07-657-769B-38

28	11	55.0	5	1	US-07-657-769B-39	Sequence 39, Appl
29	11	55.0	5	1	US-07-801-388-5	Sequence 5, Appl
30	11	55.0	5	1	US-07-792-259-9	Sequence 9, Appl
31	11	55.0	5	1	US-07-858-842-3	Sequence 3, Appl
32	11	55.0	5	1	US-07-893-930-1	Sequence 1, Appl
33	11	55.0	5	1	US-07-893-930-2	Sequence 2, Appl
34	11	55.0	5	1	US-07-893-930-3	Sequence 3, Appl
35	11	55.0	5	1	US-07-893-930-4	Sequence 4, Appl
36	11	55.0	5	1	US-07-893-930-5	Sequence 5, Appl
37	11	55.0	5	1	US-07-893-930-6	Sequence 6, Appl
38	11	55.0	5	1	US-07-893-930-7	Sequence 7, Appl
39	11	55.0	5	1	US-07-893-930-8	Sequence 8, Appl
40	11	55.0	5	1	US-07-893-930-9	Sequence 9, Appl
41	11	55.0	5	1	US-07-893-930-10	Sequence 10, Appl
42	11	55.0	5	1	US-07-893-930-11	Sequence 11, Appl
43	11	55.0	5	1	US-07-893-930-12	Sequence 12, Appl
44	11	55.0	5	1	US-07-893-930-13	Sequence 13, Appl
45	11	55.0	5	1	US-07-893-930-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-08-424-957-4

Sequence 4, Application US/08424957

Patent No. 570377

GENERAL INFORMATION:

APPLICANT: Picklesley, Steven M.

APPLICANT: Lane, David P.

TITLE OF INVENTION: Interruption of Binding of MDM2 and p53

TITLE OF INVENTION: Protein and Therapeutic Application Thereof

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hombach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/424,957

FILING DATE: 19-Apr-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/277,660

FILING DATE: 20-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-61228/WHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

US-08-424-957-4

Query Match

Best Local Similarity 70.0%;

Matches 4; Conservative 0;

Mismatches 1; Indels 0;

Score 14; DB 1; Length 5;

Pred. No. 1.9e+05;

Matches 4; Conservative 0;

Mismatches 1; Indels 0;

Score 14; DB 1; Length 5;

Pred. No. 1.9e+05;

Matches 4; Conservative 0;

Mismatches 1; Indels 0;

Score 14; DB 1; Length 5;

Pred. No. 1.9e+05;

Matches 4; Conservative 0;

Mismatches 1; Indels 0;

Score 14; DB 1; Length 5;

Db 1 FXXLM 5

RESULT 2

US-08-424-957-5

; Sequence 5, Application US/08424957

; Patent No. 570377

; GENERAL INFORMATION:

; APPLICANT: Picklesley, Steven M.

; APPLICANT: Lane, David P.

; TITLE OF INVENTION: Interruption of Binding of MD2 and P53

; TITLE OF INVENTION: Protein and Therapeutic Application Thereof

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: United States

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/424,957

; FILING DATE: 19-APR-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/277,660

; FILING DATE: 20-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Walter H.

; REGISTRATION NUMBER: 24,190

; REFERENCE/DOCKET NUMBER: A-61228/WHD

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; US-08-424-957-5

; Query Match

; Best Local Similarity 70.0%; Score 14; DB 1; Length 5;

; Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

; Oy 1 FXXW 5

; Db 1 FXXLM 5

; RESULT 3

; US-08-981-122-37

; Sequence 37, Application US/08981122B

; Patent No. 6127339

; GENERAL INFORMATION:

; APPLICANT: Hatanaka, Yoshihiro

; APPLICANT: Aritomi, Masaharu

; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/08/981,122B

; CURRENT FILING DATE: 1997-12-18

; PRIOR APPLICATION NUMBER: JP 7-176904

; PRIOR FILING DATE: 1995-06-21

; PRIOR APPLICATION NUMBER: PCT/JP96/01734

; PRIOR FILING DATE: 1996-06-21

; Query Match

; Best Local Similarity 70.0%; Score 14; DB 1; Length 5;

; Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

; Oy 1 FXXW 5

; Db 1 FXXLM 5

; RESULT 4

; US-09-035-686-4

; Sequence 4, Application US/09035686

; Patent No. 6153391

; GENERAL INFORMATION:

; APPLICANT: Picklesley, Steven M.

; APPLICANT: Lane, David P.

; TITLE OF INVENTION: Interruption of Binding of MD2 and P53

; TITLE OF INVENTION: Protein and Therapeutic Application Thereof

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: United States

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/035,686

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/424,957

; FILING DATE: 19-APR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Walter H.

; REGISTRATION NUMBER: 24,190

; REFERENCE/DOCKET NUMBER: A-61228/WHD

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; US-09-035-686-4

; Query Match

; Best Local Similarity 80.0%; Score 14; DB 4; Length 5;

; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

; Oy 1 FXXW 5

; Db 1 FXXLM 5

; RESULT 5

; US-09-035-686-4

; Sequence 4, Application US/09035686

; Patent No. 6153391

; GENERAL INFORMATION:

; APPLICANT: Picklesley, Steven M.

; APPLICANT: Lane, David P.

; TITLE OF INVENTION: Interruption of Binding of MD2 and P53

; TITLE OF INVENTION: Protein and Therapeutic Application Thereof

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: United States

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/035,686

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/424,957

; FILING DATE: 19-APR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Walter H.

; REGISTRATION NUMBER: 24,190

; REFERENCE/DOCKET NUMBER: A-61228/WHD

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; US-09-035-686-4

; Query Match

; Best Local Similarity 80.0%; Score 14; DB 4; Length 5;

; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

; Oy 1 FXXW 5

; Db 1 FXXLM 5

; RESULT 6

; US-09-035-686-4

; Sequence 4, Application US/09035686

; Patent No. 6153391

; GENERAL INFORMATION:

; APPLICANT: Picklesley, Steven M.

; APPLICANT: Lane, David P.

; TITLE OF INVENTION: Interruption of Binding of MD2 and P53

; TITLE OF INVENTION: Protein and Therapeutic Application Thereof

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: United States

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/035,686

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/424,957

; FILING DATE: 19-APR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Walter H.

; REGISTRATION NUMBER: 24,190

; REFERENCE/DOCKET NUMBER: A-61228/WHD

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; US-09-035-686-4

; Query Match

; Best Local Similarity 80.0%; Score 14; DB 4; Length 5;

; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

; Oy 1 FXXW 5

; Db 1 FXXLM 5

; RESULT 7

; US-09-035-686-4

; Sequence 4, Application US/09035686

; Patent No. 6153391

; GENERAL INFORMATION:

; APPLICANT: Picklesley, Steven M.

; APPLICANT: Lane, David P.

; TITLE OF INVENTION: Interruption of Binding of MD2 and P53

; TITLE OF INVENTION: Protein and Therapeutic Application Thereof

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: United States

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/035,686

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/424,957

; FILING DATE: 19-APR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Walter H.

; REGISTRATION NUMBER: 24,190

; REFERENCE/DOCKET NUMBER: A-61228/WHD

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; US-09-035-686-4

; Query Match

; Best Local Similarity 80.0%; Score 14; DB 4; Length 5;

; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

; Oy 1 FXXW 5

; Db 1 FXXLM 5

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FXXXW 5
1111
Db 1 FXXLW 5

RESULT 5

US-09-035-686-5

Sequence 5, Application US/09035666

Patent No. 6153391

GENERAL INFORMATION:

APPLICANT: Picklesley, Steven M.

APPLICANT: Lane, David P.

TITLE OF INVENTION: Interruption of Binding of MDN2 and P53

TITLE OF INVENTION: Protein and Therapeutic Application Thereof

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/035,686

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/424,957

FILING DATE: 19-APR-1995

APPLICATION NUMBER: US 08/277,660

FILING DATE: 20-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-61228/WHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

US-09-035-686-5

Query Match 70.0%; Score 14; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 FXXXW 5
1111
Db 1 FXELW 5

RESULT 6
US-09-099-053-3
Sequence 3, Application US/0909053
Patent No. 6388063
GENERAL INFORMATION:
APPLICANT: Greg Plowman
APPLICANT: Susan Onrust
APPLICANT: David Markby
APPLICANT: Sara Courtneidge
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: SAD RELATED DISORDERS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/099,053

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/049,914

FILING DATE: June 18, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Wardburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 235/121

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

OTHER INFORMATION: "Xaa" in position 3 stands for

OTHER INFORMATION: either Glu or Asp.

US-09-099-053-3

Query Match 70.0%; Score 14; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 FXXXW 5
1111
Db 1 FXYVW 5

RESULT 7

US-08-064-111C-22

Sequence 22, Application US/08064111C

Patent No. 5688760

GENERAL INFORMATION:

APPLICANT: Kemp, Bruce E.

APPLICANT: Nicholson, Geoffrey C.

APPLICANT: Martin, Thomas J.

APPLICANT: Fenton, Anna J.

APPLICANT: Hammonds, R. Glenn

TITLE OF INVENTION: COMPOUNDS AND COMPOSITIONS WHICH INHIBIT

TITLE OF INVENTION: BONE RESORPTION

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,111C
FILING DATE: 12-AUG-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00580
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK3879
FILING DATE: 19-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK3879
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58456/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-064-111C-22

Query Match 65.0%; Score 13; DB 1; Length 5;
Best Local Similarity 20.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
DB 1 YRSAM 5

RESULT 8
US-07-789-184-83
Sequence 83, Application US/07789184
Patent No. 5688768
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,184
FILING DATE: 19911107
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-789-184-83

Query Match 65.0%; Score 13; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
DB 1 FEFPW 5

RESULT 9
US-08-475-263-83
Sequence 83, Application US/08475263
Patent No. 5759994
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,263
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-475-263-83

Query Match 65.0%; Score 13; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
DB 1 FEFPW 5

RESULT 10
US-08-485-886-83
Sequence 83, Application US/08485886
Patent No. 5798248
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,886
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-886-83
Query Match 65.0%; Score 13; DB 1; Length 5;
Best local Similarity 40.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 FXXXW 5
DB 1 FEPFW 5
RESULT 11
US-08-477-362-83
Sequence 83, Application US/08477362
Patent No. 5849507
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,362
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-477-362-83
Query Match 65.0%; Score 13; DB 2; Length 5;
Best local Similarity 40.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 FXXXW 5
DB 1 FEPFW 5
RESULT 12
US-08-477-134-83
Sequence 83, Application US/08477134
Patent No. 5856448
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,134
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 83:

SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-477-134-83

Query Match Score 13; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
| 1
Db 1 FEPPW 5

RESULT 13
US-08-473-489A-83
Sequence 83, Application US/08473489A
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,489A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/789,184
FILING DATE: 1991-11-07
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-473-489A-83
Query Match Score 13; DB 3; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
| 1
Db 1 FEPPW 5

RESULT 14
US-08-485-695-83
Sequence 83, Application US/08485695

Patent No. 6124101
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,695
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-695-83

Query Match Score 13; DB 3; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FXXXW 5
| 1
Db 1 FEPPW 5

RESULT 15
US-08-981-122-2
Sequence 2, Application US/08981122B
Patent No. 6127339
GENERAL INFORMATION:
APPLICANT: Hatanaka, Yoshihiro
APPLICANT: Aritomi, Masaharu
TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/08/981,122B
CURRENT FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: JP 7-176904
PRIOR FILING DATE: 1995-06-21
PRIOR APPLICATION NUMBER: PCT/JP96/01734
PRIOR FILING DATE: 1996-06-21
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 5
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:

; OTHER INFORMATION: Sequence of a peptide synthesized in Example 1 from L-form
; Patent No. 6127339
; OTHER INFORMATION: F-moc amino acids by solid phase method using a multipetide
; OTHER INFORMATION: synthesizing system (Ramps)
US-08-981-122-2

Query Match 65.0%; Score 13; DB 3; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
| |
Db 1 FKIMW 5

Search completed: January 29, 2003, 14:23:38
Job time : 15 secs

